

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2005, 21:15:55 ; Search time 3504 Seconds
(without alignments)
10820.372 Million cell updates/sec

Title: US-10-688-481-6

Perfect score: 667

Sequence: 1 accccgggcgcgttagatacc.....taagagcagcagtaacgc 667

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenSmbl:1:
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_dr:*
9: gb_to:*
10: gb_strs:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hlg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	667	100.0	667 6 AR474309	AR474309 Sequence
2	667	100.0	667 6 AX282608	AX282608 Sequence
3	655	98.2	805 6 AR474304	AR474304 Sequence
4	655	98.2	805 6 AX282603	AX282603 Sequence
5	340.4	51.0	928 6 AX721083	AX721083 Sequence
6	330.4	49.5	927 15 AK099125	AK099125 Oryza sat
7	330.4	49.5	952 15 AK060332	AK060332 Oryza sat
8	329.2	49.4	945 15 AY586178	AY586178 Zea mays
9	328.8	49.3	934 15 AK099149	AK099149 Oryza sat
10	326.2	48.9	1094 15 AK112012	AK112012 Oryza sat
11	326.2	48.9	1152 15 AK103351	AK103351 Oryza sat
12	326	48.9	1035 15 AK111979	AK111979 Oryza sat
13	326	48.9	1035 15 AK119548	AK119548 Oryza sat
14	326	48.9	1049 15 AK111904	AK111904 Oryza sat
15	324.6	48.7	1086 15 AY620417	AY620417 Oryza sat
16	324.6	48.4	582 15 AF084005	AF084005 Avena fat
17	322.8	48.4	582 15 AF210431	AF210431 Nicotiana
18	320.6	48.1	957 15 TOMGTPASE	L12051 Lycopersico

19	316.4	47.4	795 15 AY070378	AY070378 Arabidops
20	316	47.4	613 15 AY117363	AY117363 Arabidops
21	312.6	46.9	884 15 AY088765	AY088765 Arabidops
22	312.6	46.9	899 15 AYU56929	AYU56929 Arabidops
23	312.6	46.9	926 15 AY065357	AY065357 Arabidops
24	311.6	46.7	613 15 AY096699	AY096699 Arabidops
25	311	46.6	709 15 AF048825	AF048825 Malus dom
26	308.2	46.2	857 15 BCU55035	BCU55035
27	305.6	45.8	1020 15 D87821	D87821 Nicotiana t
28	304.8	45.7	1031 15 BT012780	BT012780 Lycopersi
29	301.8	45.2	966 15 NPJ5AKGTP	NPJ5AKGTP
30	300.2	45.0	904 15 AY085815	AY085815 Arabidops
31	300.2	45.0	905 15 ATHGTPB	M95795 Arabidops
32	300.2	45.0	950 15 AY072220	AY072220 Arabidops
33	297.6	44.6	1013 15 NP505AR	NP505AR
34	297.2	44.6	613 15 AY096599	AY096599 Arabidops
35	292	43.8	613 15 AY090921	AY090921 Arabidops
36	291.4	43.7	829 15 BCU55036	BCU55036
37	279.4	41.9	760 15 AY620416	AY620416 Oryza sat
38	251.4	37.7	1065 15 NTSAR1	X97967 N. tabacum m
39	238.8	35.8	821 15 AK105207	AK105207 Oryza sat
40	235.2	35.3	768 15 AP424657	AP424657 Phytoph
41	218.4	32.7	421 15 NTU46928	U46928 Nicotiana t
42	216	32.4	992 6 CQ587850	CQ587850 Sequence
43	216	32.4	1512 2 BT001745	BT001745 Drosophila
44	216	32.4	3191 6 AR508145	AR508145 Sequence
45	215	32.2	380 15 NPCTPP	Y08221 N. plumbagin

ALIGNMENTS

RESULT 1
AR474309
LOCUS AR474309 667 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 6 from patent US 6689939.
ACCESSION AR474309
VERSION AR474309.1 GI:42713157
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 667)
AUTHORS da Costa e Silva, O., Bohnert, H. J., van Thiel, N. and Chen, R.
TITLE GTP binding stress-related proteins and methods of use in plants
JOURNAL Patent: US 6689939-A 6 10-FEB-2004;
BASF Plant Science GmbH; Ludwigshafen;
MOX;

FEATURES

source Location/Qualifiers
1..667
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 667; DB 6; Length 667;

Best Local Similarity 100.0%; Pred. No. 1.3e-193; Indels 0; Gaps 0;

Matches 667; Conservative 0; Mismatches 0;

QY	1	ATCCCGGGTCCGTAGATACCAAGCTGTACCAATGTTCTTGTAGATTGGTTTACGGCT	60
DB	1	ATCCCGGGTCCGTAGATACCAAGCTGTACCAATGTTCTTGTAGATTGGTTTACGGCT	60
QY	61	TTCTTTCGAGCATAGGGCTGTGCAAGAAGAGCCAAAATCTGTTCTGGGCTCGACA	120
DB	61	TTCTTTCGAGCATAGGGCTGTGCAAGAAGAGCCAAAATCTGTTCTGGGCTCGACA	120
QY	121	ATGCTGCAAGACTACTTCTTGACATGCTCAAGGATGAGAACTGGGGCAATCAAC	180
DB	121	ATGCTGCAAGACTACTTCTTGACATGCTCAAGGATGAGAACTGGGGCAATCAAC	180
QY	181	CAACGAGATATCCCAAGCTGAGAGAGTGAATCAACAGAGTGAAGTTCG	240
DB	181	CAACGAGATATCCCAAGCTGAGAGAGTGAATCAACAGAGTGAAGTTCG	240

QY 241 ATCTGGTGGCCACACATCGCTCGACGCGGTGTGGAGGACTACTATGCTTAAGGTGATG 300
DB 241 ATCTGGTGGCCACACATCGCTCGACGCGGTGTGGAGGACTACTATGCTTAAGGTGATG 300
QY 301 CTATAGTGTATCTCTGTCGACGCGCTGTAACAGGAGATTTTCTGAGTCAAGAAAGAGC 360
DB 301 CTATAGTGTATCTCTGTCGACGCGCTGTAACAGGAGATTTTCTGAGTCAAGAAAGAGC 360
QY 361 TCGATTCCTCTCTCGACGAGTCTCTGTCCCAAGTTCCGTGTCTGTCTGTGGGAAACA 420
DB 361 TCGATTCCTCTCTCGACGAGTCTCTGTCCCAAGTTCCGTGTCTGTGTGGGAAACA 420
QY 421 AGATTGATATCCCGTACGCTCTCTCTGAAGAAGAGTTGCGGTTCACTTGGGTTGACA 480
DB 421 AGATTGATATCCCGTACGCTCTCTCTGAAGAAGAGTTGCGGTTCACTTGGGTTGACA 480
QY 481 TGACCACTGTGTAAGAAAGCGGTGAACCTGGAGATAGCAACATTCGCGCCATTGAGGTTT 540
DB 481 TGACCACTGTGTAAGAAAGCGGTGAACCTGGAGATAGCAACATTCGCGCCATTGAGGTTT 540
QY 541 TCATGTGAGTATTTGTGGCAAAATGGGTTACGGTGAAGTTTCAAGTGAATGACCCAGT 600
DB 541 TCATGTGAGTATTTGTGGCAAAATGGGTTACGGTGAAGTTTCAAGTGAATGACCCAGT 600
QY 601 ACATCAAGTATTTGTTTCTCTGTGAAGAAGAGACTTACCTCGGTGTTTAAGAGCGAG 660
DB 601 ACATCAAGTATTTGTTTCTCTGTGAAGAAGAGACTTACCTCGGTGTTTAAGAGCGAG 660
QY 661 TTTAAGC 667
DB 661 TTTAAGC 667

RESULT 2
AX282608
LOCUS AX282608 667 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 6 from Patent WO0177161.
ACCESSION AX282608
VERSION AX282608.1 GI:16609685
KEYWORDS
SOURCE Physcomitrella patens
ORGANISM Physcomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryophidae; Funariidae; Funariales; Funariaceae; Physcomitrella.

REFERENCE 1
AUTHORS da Costa e Silva, O., Bohner, H.J., van Thiel, N. and Chen, R.
TITLE GTP binding stress-related proteins and methods of use in plants
JOURNAL Patent: WO 0177161-A 6 18-Oct-2001;
BASF Plant Science GmbH (DE)
FEATURES
source 1. 667
/organism="Physcomitrella patens"
/mol_type="unassigned DNA"
/db_xref="taxon:3218"

ORIGIN

Query Match 100.0%; Score 667; DB 6; Length 667;

Best Local Similarity 100.0%; Pred. No. 1,3e-193; Indels 0; Gaps 0;

Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCCCGGATCCGTAGATACCAAGGCTGTACCAATGTTCTGTAGATTGTTTACGGCT 60
DB 1 ATCCCGGATCCGTAGATACCAAGGCTGTACCAATGTTCTGTAGATTGTTTACGGCT 60
QY 61 TTCTTGGAGCATAGGCTGTGGCAAGAGGCCAAATCTGTTTCTGGGTTCTGACA 120
DB 61 TTCTTGGAGCATAGGCTGTGGCAAGAGGCCAAATCTGTTTCTGGGTTCTGACA 120
QY 121 ATGCTGCAAGACTACTCTTCTGCAATGCTCAAGATGAGAACTGGGCGCAATCAAC 180
DB 121 ATGCTGCAAGACTACTCTTCTGCAATGCTCAAGATGAGAACTGGGCGCAATCAAC 180

QY 181 CAACGAGTATCCCAAGCTCAGAGAGTTGATATCAACAGATGAATTCAAGCATTCG 240
DB 181 CAACGAGTATCCCAAGCTCAGAGAGTTGATATCAACAGATGAATTCAAGCATTCG 240
QY 241 ATCTGGTGGCCACACATGCTCTGACGCGGTGTGGAGGACTACTATGCTTAAGGTGATG 300
DB 241 ATCTGGTGGCCACACATGCTCTGACGCGGTGTGGAGGACTACTATGCTTAAGGTGATG 300
QY 301 CTATAGTGTATCTCTGTCGACGCGCTGTAACAGGAGATTTTCTGAGTCAAGAAAGAGC 360
DB 301 CTATAGTGTATCTCTGTCGACGCGCTGTAACAGGAGATTTTCTGAGTCAAGAAAGAGC 360
QY 361 TCGATTCCTCTCTCGACGAGTCTCTGTCCCAAGTTCCGTGTCTGTGTGGGAAACA 420
DB 361 TCGATTCCTCTCTCGACGAGTCTCTGTCCCAAGTTCCGTGTCTGTGTGGGAAACA 420
QY 421 AGATTGATATCCCGTACGCTCTCTCTGAAGAAGAGTTGCGGTTCACTTGGGTTGACA 480
DB 421 AGATTGATATCCCGTACGCTCTCTCTGAAGAAGAGTTGCGGTTCACTTGGGTTGACA 480
QY 481 TGACCACTGTGTAAGAAAGCGGTGAACCTGGAGATAGCAACATTCGCGCCATTGAGGTTT 540
DB 481 TGACCACTGTGTAAGAAAGCGGTGAACCTGGAGATAGCAACATTCGCGCCATTGAGGTTT 540
QY 541 TCATGTGAGTATTTGTGGCAAAATGGGTTACGGTGAAGTTTCAAGTGAATGACCCAGT 600
DB 541 TCATGTGAGTATTTGTGGCAAAATGGGTTACGGTGAAGTTTCAAGTGAATGACCCAGT 600
QY 601 ACATCAAGTATTTGTTTCTCTGTGAAGAAGAGACTTACCTCGGTGTTTAAGAGCGAG 660
DB 601 ACATCAAGTATTTGTTTCTCTGTGAAGAAGAGACTTACCTCGGTGTTTAAGAGCGAG 660
QY 661 TTTAAGC 667
DB 661 TTTAAGC 667

RESULT 3
AR474304/c
LOCUS AR474304 805 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1 from patent US 6689939.
ACCESSION AR474304
VERSION AR474304.1 GI:42713152
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1
AUTHORS da Costa e Silva, O., Bohner, H.J., van Thiel, N. and Chen, R.
TITLE GTP binding stress-related proteins and methods of use in plants
JOURNAL Patent: US 6689939-A 1 10-FEB-2004;
BASF Plant Science GmbH; Ludwigshafen;
WOX;

FEATURES
source 1. 805
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 98.2%; Score 655; DB 6; Length 805;

Best Local Similarity 100.0%; Pred. No. 6,4e-190; Indels 0; Gaps 0;

Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCGGTCGTAGATACCAAGGCTGTACCAATGTTCTGTAGATTGTTTACGGCTTCT 64
DB 781 CCGGTCGTAGATACCAAGGCTGTACCAATGTTCTGTAGATTGTTTACGGCTTCT 722
QY 65 TGGCAGCATAGGCTGTGGCAAGAGGCCAAATCTGTTTCTGGGTTCTGACAATGC 124
DB 721 TGGCAGCATAGGCTGTGGCAAGAGGCCAAATCTGTTTCTGGGTTCTGACAATGC 662
QY 125 TGGCAAGACTACTCTTCTGCAATGCTCAAGATGAGAACTGGGCGCAATCAAC 184
DB 125 TGGCAAGACTACTCTTCTGCAATGCTCAAGATGAGAACTGGGCGCAATCAAC 184

Db 661 TGCGAAGACTACTCTTCTGCAACATGCTCAAGATGAGAACTGGGGCAACATCAACCAAC 602
Qy 185 GCAGTATCCCAAGCTCAGAGAGAGTTGATATCAACAGTGAAGTTCAACATTCATCT 244
Db 601 GCAGTATCCCAAGCTCAGAGAGAGTTGATATCAACAGTGAAGTTCAACATTCATCT 542
Qy 245 GGGTGGCCACACAACTGCTGACGCGGTGGAGGAGCTTACTATGCTTAAGTGATCTAT 304
Db 541 GGGTGGCCACACAACTGCTGACGCGGTGGAGGAGCTTACTATGCTTAAGTGATCTAT 482
Qy 305 AGTGTATCTGCTGACGCACTGACAGAGAGAGATTTGCTGAGTCAAAAGAAAGCTCGA 364
Db 481 AGTGTATCTGCTGACGCACTGACAGAGAGAGATTTGCTGAGTCAAAAGAAAGCTCGA 422
Qy 365 TTCTCTTCTCTCGACGATTTCTGTCTCCAAAGTTCTGTCTGTCTGTCTGTGGAAACAAAT 424
Db 421 TTCTCTTCTCTCGACGATTTCTGTCTCCAAAGTTCTGTCTGTCTGTCTGTGGAAACAAAT 362
Qy 425 TGATATCCCGTACGCTTCTTCTGAAAGAGAGTTGCGGTTCACATTTGGTTCACATGAC 484
Db 361 TGATATCCCGTACGCTTCTTCTGAAAGAGAGTTGCGGTTCACATTTGGTTCACATGAC 302
Qy 485 CACTGTAAAGAAAGCTGTAACCTGGAGATAGCAATTCGCGCCATTGAGGTTTCAT 544
Db 301 CACTGTAAAGAAAGCTGTAACCTGGAGATAGCAATTCGCGCCATTGAGGTTTCAT 242
Qy 545 GTGCAGTATTTGTGCGCAAAATGGGGTACGCTGAAGTTTCAAGTGATGACCCAGTACAT 604
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Qy 605 CAAGTATTTGTTTCTCTGTGAAGAGAACTTAGCTGGTGTAAAGAGGACGA 659
Db 181 CAAGTATTTGTTTCTCTGTGAAGAGAACTTAGCTGGTGTAAAGAGGACGA 127

RESULT 4
AX282603/c 805 bp DNA linear PAT 02-NOV-2001
LOCUS AX282603
DEFINITION Sequence 1 from Patent WO0177161.
ACCESSION AX282603
VERSION AX282603.1 GI:16609680
KEYWORDS
SOURCE
ORGANISM
Phycomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariaceae; Funariaceae; Funariaceae; Phycomitrella.

REFERENCE
AUTHORS 1
TITLES da costa e Silva,O., Bohner,H.J., van Thiel,N. and Chen,R.
JOURNAL Gp binding stress-related proteins and methods of use in plants
BASF Plant Science GmbH (DE)
Patent: WO 0177161-A 1 18-OCT-2001;
Location/Qualifiers
1. 805
/organism="Phycomitrella patens"
/mol_type="unassigned DNA"
/db_xref="taxon:3218"

ORIGIN
Query Match 98.2%; Score 655; DB 6; Length 805;
Best Local Similarity 100.0%; Pred. No. 6,4e-190; Indels 0; Gaps 0;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGGGTCCGTAGATACCAAGGCTGTGACCATGTTTCTGTAGATTGTTTACGGCTTTCT 64
Db 781 CGGGTCCGTAGATACCAAGGCTGTGACCATGTTTCTGTAGATTGTTTACGGCTTTCT 722
Qy 65 TGGCAGCTAGAGGCTGTGAGAGAGAGGCGCAAAATCTGTTTCTGAGTCTCGAATGTC 124
Db 721 TGGCAGCTAGAGGCTGTGAGAGAGAGGCGCAAAATCTGTTTCTGAGTCTCGAATGTC 662
Qy 125 TGGCAAGACTACTCTTCTGACATGCTCAAGATGAGAACTGGGGCAACATCAACCAAC 184
Db 661 TGGCAAGACTACTCTTCTGACATGCTCAAGATGAGAACTGGGGCAACATCAACCAAC 602

Qy 185 GCAGTATCCCAAGCTCAGAGAGAGTTGATATCAACAGTGAAGTTCAACATTCATCT 244
Db 601 GCAGTATCCCAAGCTCAGAGAGAGTTGATATCAACAGTGAAGTTCAACATTCATCT 542
Qy 245 GGGTGGCCACACAACTGCTGACGCGGTGGAGGAGCTTACTATGCTTAAGTGATCTAT 304
Db 541 GGGTGGCCACACAACTGCTGACGCGGTGGAGGAGCTTACTATGCTTAAGTGATCTAT 482
Qy 305 AGTGTATCTGCTGACGCACTGACAGAGAGAGATTTGCTGAGTCAAAAGAAAGCTCGA 364
Db 481 AGTGTATCTGCTGACGCACTGACAGAGAGAGATTTGCTGAGTCAAAAGAAAGCTCGA 422
Qy 365 TTCTCTTCTCTCGACGATTTCTGTCTCCAAAGTTCTGTCTGTCTGTCTGTGGAAACAAAT 424
Db 421 TTCTCTTCTCTCGACGATTTCTGTCTCCAAAGTTCTGTCTGTCTGTCTGTGGAAACAAAT 362
Qy 425 TGATATCCCGTACGCTTCTTCTGAAAGAGAGTTGCGGTTCACATTTGGTTCACATGAC 484
Db 361 TGATATCCCGTACGCTTCTTCTGAAAGAGAGTTGCGGTTCACATTTGGTTCACATGAC 302
Qy 485 CACTGTAAAGAAAGCTGTAACCTGGAGATAGCAATTCGCGCCATTGAGGTTTCAT 544
Db 301 CACTGTAAAGAAAGCTGTAACCTGGAGATAGCAATTCGCGCCATTGAGGTTTCAT 242
Qy 545 GTGCAGTATTTGTGCGCAAAATGGGGTACGCTGAAGTTTCAAGTGATGACCCAGTACAT 604
Db 241 GTGCAGTATTTGTGCGCAAAATGGGGTACGCTGAAGTTTCAAGTGATGACCCAGTACAT 182
Qy 605 CAAGTATTTGTTTCTCTGTGAAGAGAACTTAGCTGGTGTAAAGAGGACGA 659
Db 181 CAAGTATTTGTTTCTCTGTGAAGAGAACTTAGCTGGTGTAAAGAGGACGA 127

RESULT 5
AX721083 928 bp mRNA linear PAT 07-MAY-2003
LOCUS AX721083
DEFINITION Sequence 43 from Patent WO0220754.
ACCESSION AX721083
VERSION AX721083.1 GI:30421919
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
AUTHORS 1
TITLES Lincoln,S.E., Altus,C.M., Dufour,G.E., Chalup,M.S., Hillman,J.L.,
JONES,A., Yu,J.Y., Wright,R.J., Gietzen,D., Liu,Toomy,F., Yap,P.,
Dahl,C.R., Momiyama,M., Bradley,D., Rohatgi,S., Harris,B.,
Roseberry,A.M., Gerstein,E.H., Petralia,C.H., David,M., Panzer,S.,
Flores,V., Dafio,A., Marwaha,R., Chen,A., Chang,S.C. and Inman,R.R.
JOURNAL Molecules for diagnostics and therapeutics
Patent: WO 0220754-A 43 14-MAR-2002;
Location/Qualifiers
1. 928
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/note="Incyte ID No: LI:722913.1:2000SEP08"

ORIGIN
Query Match 51.0%; Score 340.4; DB 6; Length 928;
Best Local Similarity 74.7%; Pred. No. 4.5e-93;
Matches 441; Conservative 0; Mismatches 146; Indels 3; Gaps 1;

Qy 23 GCGTGTACATATTTCTTGTAGATTGCTTACGCTTTCTTGTGAGCATAGGGGCTG 82
Db 153 GGTGGGGAGATGTTCTCTGGAATGCTGCTGAGGAGGCTGCTCTCTGAGCTG 212
Qy 83 GCAGAGAGAGGCAAAATCTGTTTCTGAGTCTGACATGCTGCAAGACTACTCTTCT 142

Db 213 GCAGAGAGAGCCGCAAGATCTCTTCTTGCCCTGACACAGCCCGGCAAGACCAAGCTGCT 272

Qy 143 GCACATGCTCAAGAGATGAGAAATCGGGCAACATCAACCAACGAGATATCCAGCTGAGA 202

Db 273 CCACATGCTCAAGAGACGAGCGGTTGGTGACACACAGCGACGAGACCCGACGTCGGA 332

Qy 203 GGAATTGATTCACACAGAGTGAAGTTCAAGCATTCGATCTGGGTGGCCACACAAATGCC 262

Db 333 GGAGCTCAGCATCGGCAAGATCAAGTTCAAGCCGTTCACTCGCGGCGCCACGATCGC 392

Qy 263 TCGACGCGTGTGAGAGGAGCTACTATGTAGTGAAGTGGATGCTATGTATCTCGTCGACGC 322

Db 393 GCGCGCGCTGTGAGAGATTACTACGCAAGGTTGATCTATATACCTGGTAGATGC 452

Qy 323 AGTAGACAGGAGAGATTTGCTGAGTCAAGAAAGAGCTCGATTTCTTCTTCGACGA 382

Db 453 ATATGATAGAGAGGATTTGCTGATCAAGAAAGAGCTGATGCTCTCGTCTGATGA 512

Qy 383 TTCTCTGTCACAAATTTCTGCTGCTGCTGCTGCGAAACAAATTTGATCCGTCACGCTTC 442

Db 513 TTCTTTGGCCAAATGTTTCATTTCTCATCTTGGCAACAAATGATATCCCATATGCTGC 572

Qy 443 TTCTGAGACAGAGTGGCGTTCAACACTTGGGTTGACCA---TGAACCACTGGTAAAGGAC 499

Db 573 CTCTGAGAGAGAGCTACCGTATACCTTAGCCCTTAGCACTTCAACACCGGAGAGGCAA 632

Qy 500 GGTGAACCTGGAGATAGCAACATTCGCGCCCATTTGAGGTTTTCATGTGCACTATTGTGCG 559

Db 633 GGTCAACCTTGGCGAGCTCCATATGTCGTCGCACTTGAAGGTTTCAATGTGCACTATTGTTCG 692

Qy 560 CAAATGGGATTCGCTGAGAGTTTCAATGTGATGACCAAGTACATCAAGT 609

Db 693 CAAGATGGGCTACGCTGATGATGTTTCAAGTGGGCTCTCCAGTACATCAAGT 742

RESULT 6

AK099125

LOCUS DEFINITION AK099125 927 bp mRNA linear PLN 24-JUL-2003

ORYZA SATIVA (JAPONICA CULTIVAR-GROUP) cDNA clone:J023044P12, full insert sequence.

ACCESSION AK099125

VERSION AK099125.1 GI:32984334

KEYWORDS FULL_CDNA; CAP trapper.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1

AUTHORS The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team;

Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotte,I., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group, Otono,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Nikiura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN;

Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,M., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Otsu,N., Oca,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y.

TITLE Collection, mapping, and annotation of over 28,000 cDNA clones from Japonica rice

JOURNAL Science 301 (5631), 376-379 (2003)

PUBMED 12869764

REFERENCE 2 (bases 1 to 927)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,M.,

Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hirooka,T., Horii,F., Hotte,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K., Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Koude,M., Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Nikiura,J., Nishi,K., Nomura,K., Numasaki,R., Ohtsuki,K., Oka,M., Ooka,H., Otsu,N., Oca,Y., Otono,Y., Ryu,R., Satoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akashira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A.

Direct Submission

Submitted (27-AUG-2002) Shoeni Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kamondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:kikuchienas.affrc.go.jp, tel:81-29-858-7007, fax:81-29-858-7007)

This clone is one of the 28k full-length cDNA clones from japonica rice.

URL://cdna01.dna.affrc.go.jp/cdna/

NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotte,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., and Yamamoto,M.

FAIS Genome Sequencing & Analysis Group: Otono,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Nikiura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K., and Murakami,K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,M., Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Horii,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Koude,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohtsuki,N., Oca,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akashira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.

Location/Qualifiers

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/clone="J023044P12"

ORIGIN

Query Match 49.5%; Score 330.4; DB 15; Length 927;

Best Local Similarity 74.3%; Prod. No. 5.3e-90;

Matches 431; Conservative 0; Mismatches 146; Indels 3; Gaps 1;

Qy 33 ATGTTCTTGAATGCTTTTACGCGCTTCTTGCGACATTAAGGCTGTGGCAAGAGAG 92

Db 127 ATGTTCTGCTGAGACTGCTTCTACGCGGCTGCTGCGCTGCGGCTGTGTGCAAGAGAG 186

Qy 93 GCCAAAATCTGTTTCTGCGGCTTCGACAAAGCTGGCAAGACTCTCTTTCGACATGCTC 152

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 QY 453 GAGTTGGGTTCAACTTGGGTTGACCA---TGACCATGTTAAAGAAAGGATGAACTTG 509
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 QY 510 GGAGATGCAACATTCGGGCGCCATTGAGGTTTTCATGTCAGATTTGTCGCAAAATGGGG 569
 DB 607 GGGGAGTCCACGTTCCCTCGAGAGTGTTCATGTGACGATCGTCCGCAAGATGGGC 666
 QY 570 TACGCTGAAGTTTCAAGTGAATGATCCCATCAATCAATCAAGT 609
 DB 667 TATGGGATGGGTTCAAGTGGGTTGCTCACATCAATCAAGT 706

RESULT 7
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 LOCUS
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:001-008-B07, full insert sequence.
 ACCESSION AK060332
 VERSION AK060332.1 GI:32970350
 KEYWORDS Full CDNA; oligo-capping.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS 1 The Rice Full-length CDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length CDNA Project Team,

Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Ohtsuki, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN: Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Kono, H., Miyazaki, A., Otsu, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.
 Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice

TITLE Science 301 (5631), 376-379 (2003)

JOURNAL
 PUBMED 12869764
 REFERENCE
 AUTHORS 2 (bases 1 to 952)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanegaki, T., Hara, A., Hashizume, W., Hayashide, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hirooka, T.,

Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imocani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Nishikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Otsu, N., Ota, Y., Ohtsuki, K., Ryu, R., Saitoh, K., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and Yoshimura, A.
 Direct Submission
 Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
 This clone is one of the 28k full-length cDNA clones from japonica rice.

COMMENT

URL: http://cdna01.dna.affrc.go.jp/cDNA/NIAS_Rice_Full-length_cDNA_Project_Team_Kikuchi_S_Satoh_K_Ishikawa_M_Yamada_H_Ooka_H_Hotta_I_Ishikawa_M_Yamada_H_Ooka_H_Hotta_I_Kojima_K_Namiki_T_Ohneda_E_Yahagi_W_Suzuki_K_Li_C_Ohtsuki_K_Shishiki_T_and_Yamamoto_M

PAIS Genome Sequencing & Analysis Group: Ohtsuki, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nishikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.
 Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Hayatsu, N., Hiramoto, K., Hara, A., Hashizume, W., Hayashide, K., Fukuda, S., Hanegaki, T., Hirooka, T., Hori, F., Iida, J., Imamura, K., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Otsu, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.

FEATURES

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ORIGIN

Query Match 49.5%; Score 330.4; DB 15; Length 952;
 Best Local Similarity 74.3%; Pred. No. 5.3e-90;
 Matches 431; Conservative 0; Mismatches 146; Indels 3; Gaps 1;
 QY 33 ATGTTCTTGATGATTGTTTACGGCTTCTTGCAGCATAGAGCTGTGCGAAGAG 92
 DB 130 ATTCTCTGCTGACATCGTTCTTACGGGGTGTGGCTCGCTGGGCTGTGCGAAGAG 189
 QY 93 GCCAAATCTGTTTGGGCTTCGACATGCTGCGAAGACTACTCTTCTGCAATGCTC 152
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 QY 570 TACGATGAAGTTCAAGTGAATGAGCCAGTATCAAGT 609
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RESULT 8
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 LOCUS
 Zea mays putative ras-like small GTP binding protein mRNA, complete cds.
 ACCESSION
 AY596178
 VERSION
 AY596178.1 GI:4694655
 KEYWORDS
 ORGANISM
 Zea mays
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.

REFERENCE
 AUTHORS
 TITLE
 Zea mays
 Suppressing apoptosis is a key mechanism of maize S-CMS restore gene R13
 JOURNAL
 Unpublished
 REFERENCE
 2 (bases 1 to 945)
 AUTHORS
 Zhang, Z., Tang, W. and Zheng, Y.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (11-APR-2004) National Key Lab of Crop Genetic Improvement, Huangzhong Agricultural University, Wuhan, Hubei 430070, China

FEATURES
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ORIGIN

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 Best Local Similarity 73.1%; Pred. No. 1,2e-89;
 Matches 437; Conservative 0; Mismatches 158; Indels 3; Gaps 1;

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 QY 319 ACCGATGACAGAGAGAGATTGCTGAGTCAAGAAAGAGCTGATTTCTTCTCCG 378
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 QY 379 AGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 438
 DB 417 ATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 476
 QY 439 CTCTCTCTGAGAGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 495
 DB 477 CGCTTCTGAGAGAGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 536
 QY 496 GAAAGGTAACCTGGAGATGAGCAACATTCGCGCCATTGAGTTTCAATGCAATTTG 555
 DB 537 GCAACGTGAACCTGGAGATGAGCAACATTCGCGCCATTGAGTTTCAATGCAATTTG 596
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RESULT 9
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 LOCUS
 Oryza sativa (japonica cultivar-group) cdna clone:J023063C05, full insert sequence.
 DEFINITION
 AK099149
 VERSION
 AK099149.1 GI:32984358
 KEYWORDS
 FLI CDNA; CAP trapper.
 SOURCE
 Oryza sativa (japonica cultivar-group)
 ORGANISM
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS
 The Rice Full-length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA Project Team,
 Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
 Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotra, I.,
 Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
 Ohtsuki, K., Shienkai, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Otsu, Y., Murakami, K.,
 Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
 Kurogaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
 Nariwaka, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nikiura, J.,
 Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Mura, J.,
 Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN,
 Kawai, J., Carninci, P., Adachi, T., Aizawa, K., Aizawa, T., Fukuda, S.,

TITLE Hara, A., Hashidume, M., Hayaesu, N., Imotani, K., Ishii, Y., Itoh, M., Kaga, I., Kondo, S., Komno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasai, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.
JOURNAL Collection, mapping, and annotation of over 28,000 cDNA clones from Japanese rice
Science 301 (5631), 376-379 (2003)

REFERENCE
AUTHORS

2. (Bases 1 to 934)

Adachi, J., Aizawa, S., Akimura, T., Arkawa, T., Carinici, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraka, T., Horii, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Komoto, H., Kouda, M., Koya, S., Kurihara, C., Kurotsuki, T., Kusneger, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Mura, T., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Nomura, K., Numaeki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Ootao, N., Ota, Y., Otomo, Y., Ryu, R., Saichoh, A., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Saeaki, D., Sato, K., Satoh, K., Shibata, K., Shikigawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaki-Akashita, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

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FEATURES
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Matches	430;	Conservative	0;	Mismatches	147;	Indels	3;
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Db	430	GAGAGTTTCCGAGTTCGAAGAAAGAGCTCGACGCCCTCTCTCGACGACTCCCTGGCC	489
OY	393	CAAGTTCTGTGCTCGTCTCTGGGAAACAAGATTGATATCCCGTACGGCTTTCTGGAAGAC	452
Db	490	ACCGTCCCTTCTGATCTCGGGCAAGAAATGACATCCCTTACGCGCGCTCGAAGAG	549
OY	453	GAGTTGGGTTCAACTTGGGTTGACCA---TGACCACTGTTAAAGAACGATGAACCTG	509
Db	550	GAGTCCGCTACCAACATGGGGCTGAGCACTTACCAACCGGCAAGGGCAGGTGACCTC	609
OY	510	GGAATGACAACTTCGGCCCATTTGAGTTTTCATGTGCAGATATTGTGCGCAAAATGGG	569
Db	610	GGCAGTCAACGTTTCGCCCTCGAGAGTGTTCATGTGACGACATCGTCCGCAATGGGC	669
OY	570	TACGTTAAGATTCAAGTGAATGACCCAGTACTCAAGT	609
Db	670	TATGGGATGGTTCAAGTGGGTGTACCGGTACTCAAGT	709

RESULT	10				
AKI12012					
LOCUS					
DEFINITION	AKI12012	1094 bp	mRNA	linear	PLN 29-OCT-2003
	<i>Oryza sativa</i> (japonica cultivar-group)			cdna clone:006-210-H07, fulllength insert sequence.	
ACCESSION	AKI12012				
VERSION	AKI12012.1	GI:37988675			
KEYWORDS	PLI CDNA; oligo capping.				
SOURCE	<i>Oryza sativa</i> (japonica cultivar-group)				
ORGANISM	<i>Oryza sativa</i> (japonica cultivar-group)				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
	Eleusineaceae; Oryzaceae; Oryza.				
REFERENCE	1				

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AUTHORS

1. The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yabagi, W., Suzuki, K., Li, C., Ohtsuka, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group, Otonari, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kuroski, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Nakikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Mikiura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Nara, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, N., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,

Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Otsu, N., Ota, Y.,
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Yoshino, M. and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)
12869764

JOURNAL
PUBMED
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AUTHORS

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Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J.,
Yokomizo, S. and Yoshimura, A.
Rice full-length cDNA
Unpublished
3 (bases 1 to 1094)
Kikuchi, S.
Direct Submission
Submitted (12-SEP-2002) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
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305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 32k full-length cDNA clones from japonica
rice.
URL : <http://cdna01.dna.affrc.go.jp/cDNA/>
NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
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Yamamoto, M. and Nakahama, Y.
PLS Genome Sequencing & Analysis Group: Otsu, Y., Iida, Y.,
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Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M.,
Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
Takaki-Akahita, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
Yasunishi, A. and Hayashizaki, Y.

FEATURES
SOURCE

1. 1094
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultiVar="Nipponbare"

ORIGIN
Query Match 48.9%; Score 326.2; DB 15; Length 1094;
Best local Similarity 72.0%; Pred. No. 1,1e-88;
Matches 440; Conservative 0; Mismatches 168; Indels 3; Gaps 1;
/db_xref="taxon:39947"
/clone="006-210-H07"

QY 2 TCCGGGCGCGTAGATACCAAGGCTGTACCATGTTCTTTGATGATTGTTTACGCGCTT 61
DB 183 TACAGAGAGAGAAAGAGCGCGGAGAGAGAAAGATGTTCTGTGGAGCTTTCACGCGCT 242
QY 62 TCTTGGAGACATPAGGCTGTGCGAAGAGAGAGCGCAAAATCTGTTCTGGGTCTGACAA 121
DB 243 GCTCGGCTGCTGGGCTGTGGAGAGAGAGCGCAAGATCTTCTTCTGGCTTCACAA 302
QY 122 TGTGGCAAGACTACTCTTCTGACATGTCTCAAGATGAGAACTGGGGCAATCAAC 181
DB 303 CGCGGCAAGACCACTCTCTCTCAATGCTCAAGAGAGAGAGATTTGTCAGCACAGCC 362
QY 182 AACGAGATTCACAGCTCAGAGAGAGTGTATCAACAGATGAAGTTCAAGCATTCGA 241
DB 363 GACGAGACACCGAGCGTGGAGAGCTCAGCATCGGAAAGATCAAGTTCAAGGCTTCGA 422
QY 242 TCTGGGTGGCCACACATGCTGAGCGGTGGAGAGACTACTATGCTTAAGTGAATGC 301
DB 423 TCTCGGCGGCAACAGATGCGCGCGCTGTGGAAGACTACTACGCCAAGGTTATGC 482
QY 302 TATAGTGTATCTGTCGACGAGATGACAGAGAGAGATTTGCTGAGTCAAGAAAGAGCT 361
DB 483 TGTGTATATTTGTGTAGATGCTTATGATTAAGAACTTTTCTGATTCAAAAAGAGCT 542
QY 362 CGATTCCTTCTCTCGAGAGATTCCTGTCCAAAGTTCTGTGCTCTGCGGAAAAACA 421
DB 543 TGAATGACCTCTATGATGATTCATTTGAGAGCTGCCGTTCTTATCTTGGCAACAA 602
QY 422 GATTGATTCCTGATGCTTCTTCTGAAGACAGATTTGCGGTTCACACTTGGGTGACCA 480
DB 603 GATTGACATTCATGATGCTTCTTGAAGAGAGCTGCGGTATCATCTAGGCTTGACAA 662
QY 481 --TGACCACTGGAAAGAAACGCTGAACCTGGAGATGACCAATTCGCGCCATTGAGGT 538
DB 663 CTTCACAACTGGAGAGAGAGAGCTGAGCTTATGATGATTCATTCGCGCCCTCGAAGT 722
QY 539 TTTTCATGTGAGATTTGTGGCAAAATGGGGTACGCTGAAGGTTTCAAGTGAAGACCA 598
DB 723 GTTCATGTGAGATTTGTGGCAAAATGGGGTATGAGACGAGTTCAAGTGGGTCTCCCA 782
QY 599 GTTCAATCAAGT 609
DB 783 GTACATCAAGT 793

RESULT 11
AKI03351
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone:U033126116, full
insert sequence.
ACCESSION
AKI03351
VERSION
AKI03351.1 GI:32988560
KEYWORDS
Oryza sativa (japonica cultivar-group)
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS
1 The Rice Full-length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-length cDNA Project Team,
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
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Ohtsuki, K., Shishiki, T., Foundation of Advancement of International

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TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

Japanese rice
collection, mapping, and annotation of over 28,000 cDNA clones from
Science 301 (5631), 376-379 (2003)
12869764

TITLE
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Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J.,
Yokomizo, S., and Yoshimura, A.

COMMENT

Collection, mapping, and annotation of 28k full-length cDNA clones
from japonica rice
Unpublished
3 (bases 1 to 1035)

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

Direct Submission
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tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 32k full-length cDNA clones from japonica
rice.
URL: //cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
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FAIS Genome Sequencing & Analysis Group: Ohtomo, Y., Iida, Y.,
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Takaku-Akashira, S., Tanaka, T., Tomaru, A., Toyota, T., Waki, K.,
Yasunishi, A., and Hayashizaki, Y.

FEATURES

source

1. 1035
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="001-207-C09"

ORIGIN

Query Match 48.9%; Score 326; DB 15; Length 1035;
Best Local Similarity 73.7%; Pred. No. 1.2e-88;
Matches 429; Conservative 0; Mismatches 150; Indels 3; Gaps 1;
33 ATGTTCTGTGATGATTGTTTACGCTTTCTGAGAGATAGGGCTGGCAGAGAG 92
|||||
90 ATGTTCTGTGATGATTGTTTACGCTTTCTGAGAGATAGGGCTGGCAGAGAG 149
|||||
93 GCCAAATCTGTTTCTGAGTCTGCAAAATGCTGGCAGATCTTCTGCAATGCTC 152
150 GCCAATCTCTCTCTCTGCTGCTGCAAAATGCTGGCAGATCTTCTGCAATGCTC 209
153 AAGATGAGAAATGCGGCAATCAACCAAGCATATCCCAAGCTCAAGAGATTGACT 212
|||||
210 AAGGACGACGCTCTGTCAGACCAAGCCGACGATCCGACGTCGAGAGAGCTGACC 269
213 ATCAACAGATGAGTCAAGATTCGATCTGAGGCGCCACCAATGCTGACGCTG 272
270 ATGCGCAATCAAGTCAAGGCTTTCGACTTGGGCGCCACCAATGCTGACGCTG 329
273 TCGAGGACTACTATGCTAAGTGTGATAGTATCTGCTGACGACGATGAGACAG 332
330 TCGAAGGACTACTATGCTAAGTGTGATAGTATCTGCTGACGACGATGAGACAG 389
333 GAGAGATTGCTGAGTCAAAAGAAAGCTGATCTCTTCTCTCCAGCATTTCTGTCTC 392
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393 CAAGTCTCTGCTGCTGCTGCTGAGAAACAGATTCATCCGATGCTTCTGAGAC 452
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570 GCGCACTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 629
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630 TACGCGGAGAGCTTCAATGAGATGCTCCAGTACATCAATGAG 671
RESULT 14
AK111904 1049 bp mRNA linear PLN 29-OCT-2003
LOCUS AK111904
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone: J023112P13, full
insert sequence.
ACCESSION AK111904
VERSION AK111904.1 GI:37988567
KEYWORDS FLI_CDNA; CAP trapper.

SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS

1
The Rice Full-length cDNA Consortium, National Institute of
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Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, K., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
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Japonica rice
Science 301 (5631), 376-379 (2003)
12869764

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

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Xie, Q., Yanagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J.,
Yokomizo, S. and Yoshimura, A.

TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL

3
Rice full-length cDNA
Unpublished
3 (bases 1 to 1049)
Kikuchi, S.
Submitted
Direct Submission
Submitted (12-SEP-2002) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression, 2-1-2 Kamondoai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp).
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 32k full-length cDNA clones from japonica
rice.
URL : http://cdna01.dna.affrc.go.jp/cdna/
NIRS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, K.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
Ohneda, E., Yanagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shiehiki, T.,
Yamamoto, M. and Nakahama, Y.
FAIS Genome Sequencing & Analysis Group: Otsu, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Kurosaki, T., Kusunegi, T., Lu, M.,
Kobayashi, M., Kodama, T., Kurosaki, T., Nishikura, J., Oka, M.,
Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nishikura, J., Oka, M.,
Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M.,
Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.

COMMENT

Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hashidume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
Hirooka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kouda, M.,
Koya, S., Kurihara, C., Kurosaki, T., Kusunegi, T., Li, C., Lu, M.,
Masuda, H., Matsubara, K., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Otsu, N.,
Ota, Y., Saitoh, H., Sakai, C., Sakai, K.,
Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K.,
Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M.,
Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
Takaku-Akashita, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
Yasunishi, A. and Hayashizaki, Y.
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/clone="J023112P13"

ORIGIN

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Best Local Similarity 73.7%; Pred. No. 1,2e-88;
Matches 429; Conservative 0; Mismatches 150; Indels 3; Gaps 1;

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RESULT 15
AY620417 1086 bp mRNA linear PLN 24-MAY-2004
LOCUS AY620417
DEFINITION Oryza sativa (japonica cultivar-group) clone P0705D01 GTP-binding

protein (GBP) mRNA, complete cds.

ACCESSION AY620417
VERSION AY620417.1 GI:47499877

KEYWORDS

Oryza sativa (japonica cultivar-group)

SOURCE

Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriarctideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 1086)
Weng, X.-B., Lin, R.-M., Wang, M., Zhao, W.-S. and Peng, Y.-L.
Molecular cloning and expression of a Magnaporthe grisea induced
cDNA encoding a small GTP-binding protein

TITLE

JOURNAL

2 (bases 1 to 1086)
Weng, X.-B., Lin, R.-M., Wang, M., Zhao, W.-S. and Peng, Y.-L.
Direct Submission
Submitted (21-APR-2004) Plant Pathology, China Agricultural
University, West Road No. 2 of Yuanmingyuan Haidian, Beijing,
Beijing 100094, China

JOURNAL

Location/Qualifiers
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FEATURES

source

1. .1086
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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ADSNVRPLRIFMCSVVRKMGYEGFKMSQYIK"

gene

CDS

ORIGIN

Query Match 48.9%; Score 326; DB 15; Length 1086;
Best Local Similarity 73.7%; Pred. No. 1,2e-88;
Matches 429; Conservative 0; Mismatches 150; Indels 3; Gaps 1;

33 ATGTTCTGTAGATTGTTTACGGCTTCTTGCGAGCATAGGGCTGTGGCAGAAAGAG 92
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93 GCCAAATCTGTTTCTGGGCTCTGACATAGCTGGCAAGACTACTTCTTGACATGCTC 152
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417 ACCGTGCTTCTTCTGATCTGGAACCAAGTGCATCCCATACGCCGCTGAGAGAG 476

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
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Searched: 4996997 seqs, 3332346308 residues
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Minimum DB seq length: 0
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Listing first 45 summaries

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- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	667	100.0	667	13	ADT91569	Adt91569 Physcomit
3	655	98.2	805	6	ABN89809	ABN89809 Physcomit
4	655	98.2	805	13	ADT91564	Adt91564 Physcomit
5	340.4	51.0	928	6	ABK71577	Abk71577 Human dit
6	340.4	51.0	998	13	ADK12667	Adk12667 Plant ful
7	335.6	50.3	955	13	ADK46899	Adk46899 Plant ful
8	332.4	49.8	966	13	ADK30716	Adk30716 Plant ful
9	332.4	49.8	1017	13	ADK62517	Adk62517 Plant ful
10	331.2	49.7	811	11	ADK45502	Adk45502 Insect re
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23	317.4	47.6	615	11	ADK45777	Adk45777 Insect re
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26	312.6	46.9	885	3	AAK42538	AAK42538 Arabidops
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28	310	46.5	680	11	ADK44921	Adk44921 Insect re
29	310	46.5	689	11	ADK45514	Adk45514 Insect re
30	310	46.5	689	11	ADK45782	Adk45782 Insect re
31	303.4	45.5	1102	11	ACL132345	ACL132345 Rice abio
32	300.2	45.0	904	3	AAK36976	AAK36976 Arabidops
33	296.6	44.5	592	13	ACN60391	ACN60391 Cotton gy
34	295	44.2	675	6	ABO65802	ABO65802 Arabidops
35	294.2	44.1	640	11	ADK44923	Adk44923 Insect re
36	294.2	44.1	669	11	ADK45787	Adk45787 Insect re
37	294.2	44.1	669	11	ADK45518	Adk45518 Insect re
38	292	43.8	582	3	AAK42867	AAK42867 Arabidops
39	272.6	40.9	569	13	ACN48893	ACN48893 Cotton pr
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41	267.2	40.1	677	11	ADK45802	Adk45802 Insect re
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44	262.8	39.4	603	13	ACN56676	ACN56676 Cotton gy
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ALIGNMENTS

RESULT 1	ABN89814	standard; cDNA, 667 BP.
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XX	ABN89814	
DT	18-SEP-2002	(first entry)
XX	ABN89814	
DE	Physcomitrella patens	GBP-1 encoding cDNA sequence SEQ ID NO:6.
XX	Physcomitrella patens	GBP; GTP binding protein; GBSRP; plant;
KW	GTP binding stress-related protein; transgenic plant; agricultural;	
KM	environmental stress; salinity; drought; temperature; gene; ss.	
XX	Physcomitrella patens.	
OS	Physcomitrella patens.	
XX	Physcomitrella patens.	
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XX	30-MAY-2002.	
XX	06-APR-2001, 2001US-00828310.	
XX	07-APR-2000, 2000US-0196001P.	
XX	(SILV/) SILVA O D C E.	
PA	(BOHN/) BOHNERT H J.	
PA	(THIE/) THIELEN N V.	
PA	(CHEN/) CHEN R.	
XX	Silva ODCE, Bohnert HJ, Thiele N, Chen R;	
PI	WPI: 2002-556781/59.	
DR	P-PDB; ABB81583.	
XX	Novel GTP binding stress-related proteins and genes encoding the	
PT	proteins, useful for producing transgenic plants having increased	
PT	tolerance to environmental stress as compared to wild type variety of	

PT plant cell.

XX Claim 16; Fig 2a; 73pp; English.

XX
 CC The present invention describes an isolated GTP binding stress-related
 CC protein (GBSRP) (I) from *Physcomitrella patens*, selected from GTP binding
 CC protein-1 (GBP-1), GBP-2, GBP-3, GBP-4 and GBP-5, or its orthologues. (I)
 CC can be used for producing a transgenic plant (e.g., maize, wheat, rice,
 CC oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola,
 CC manihot, pepper, sunflower, tagetes, solanaceous plants, potato, tobacco,
 CC eggplant, tomato, *Vicia* species, pea, alfalfa, coffee, cacao, tea, *Salix*
 CC species, oil palm, coconut, perennial grass and forage crops). The
 CC transgenic plants produced have increased tolerance to environmental
 CC stress (e.g., salinity, drought and temperature) as compared to a wild
 CC type variety of the plant, from the plant cell. GBSRP polynucleotide
 CC sequences can be used as markers for specific regions of the genome, and
 CC also in functional studies of *P. patens* proteins. They can also be used
 CC for evolutionary and protein structural studies. The present sequence
 CC encodes the *P. patens* GBP-1 protein, which is used in the exemplification
 CC of the present invention

XX Sequence 667 BP; 169 A; 142 C; 185 G; 171 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 667; DB 6; Length 667;

XX Best Local Similarity 100.0%; Pred. No. 4.1e-220;

XX Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATCCCGGAGTCGATGATACCAAGGCTGTGATCATGTTCTTGTAGATTGGTTTACGGCT 60

QY 61 TTCTTGGAGCATAGGGCTGTGGAGAGAGGCAAAATCTGTTCTGGGTTCTGACA 120

Db 61 TTCTTGGAGCATAGGGCTGTGGAGAGAGGCAAAATCTGTTCTGGGTTCTGACA 120

QY 121 ATGCTGGCAAGACTACTCTTCTGACATGCTCAAGATGAGAACTGGGGCAATCAAC 180

Db 121 ATGCTGGCAAGACTACTCTTCTGACATGCTCAAGATGAGAACTGGGGCAATCAAC 180

QY 121 ATGCTGGCAAGACTACTCTTCTGACATGCTCAAGATGAGAACTGGGGCAATCAAC 180

Db 121 ATGCTGGCAAGACTACTCTTCTGACATGCTCAAGATGAGAACTGGGGCAATCAAC 180

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QY 301 CTATAGGTATCTGTGAGAGCATATGACAGAGAGATTTGCTGAGTCAAAAGAAAGC 360

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QY 361 TCGATTCTCTCTCCGACGATTCCTGTCCTCAAGTTCTCTGCTCGCTCGGAGAAACA 420

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QY 421 AGATTGATATCCCGTAGCGTCTTCTGAAAGCAAGTTGCGGTTTCACTTGGGTTGACA 480

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QY 481 TGACCACTGTGTAAGAAAGGTAAGCTGGAGATGAGCAATTCGGCCCAATTAGGTTT 540

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QY 541 TCATGTGCAATGATGTTGTCGCAAAATGGGTAAGGTTTCAAGTGATGACCGAGT 600

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QY 601 ACATCAAGTATGTTTCTCTGTGAAAGAGAACTTAACTCGTGTGTTTAAAGCAGAG 660

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QY 601 ACATCAAGTATGTTTCTCTGTGAAAGAGAACTTAACTCGTGTGTTTAAAGCAGAG 660

Db 601 ACATCAAGTATGTTTCTCTGTGAAAGAGAACTTAACTCGTGTGTTTAAAGCAGAG 660

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Db 661 TTAACGC 667

QY 661 TTAACGC 667

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Db 661 TTAACGC 667

RESULT 2

ADT91569 standard; cDNA; 667 BP.

XX ADT91569;

DT 16-DEC-2004 (first entry)

DE *Physcomitrella patens* GBP full-length cDNA, PgGBP-1.

XX GTP-binding stress-related protein; GBSRP; transgenic plant;

KM environmental stress tolerance; stress resistance; cell metabolism;

KM GTP binding protein; GBP; gene; ss.

OS *Physcomitrella patens*.

FH Key Location/Qualifiers

FT CDS 33..611

FT /tag= a

FT /product= "PgGBP-1 protein"

PN US2004194163-A1.

PD 30-SEP-2004.

XX 17-OCT-2003; 2003US-00688481.

XX 07-APR-2000; 2000US-0196001P.

PR 06-APR-2001; 2001US-00828310.

XX (BADI) BASF PLANT SCI GMBH.

PI Da Costa E Silva, Bohnert HJ, Thielens NV, Chen R;

XX WPI; 2004-698822/68.

DR P-PSDB; ADT91574.

XX Novel isolated nucleic acid encoding polypeptide e.g., GTP-binding stress

PT -related protein, useful for producing vector utilized for producing

PT transgenic plant that has increased tolerance to environmental stress.

PS Claim 12; SEQ ID NO 6; 62pp; English.

XX The invention relates to nucleic acid sequences encoding GTP-binding

CC stress-related proteins (GBSRP). GBSRP DNA is useful for producing a

CC recombinant expression vector utilized for producing a transgenic plant

CC that has increased tolerance to environmental stress, for identifying

CC *Physcomitrella patens* and related organisms, for identifying andCC localising *P. patens* sequences of interest, for evolutionary studies, for

CC determining GBSRP regions required for function, for modulating GBSRP

CC activity, for modulating metabolism of one or more cell function, for

CC modulating transport of one or more compounds, for modulating stress

CC resistance or as markers for specific regions of the genome of *P. patens*.CC The present sequence is the *Physcomitrella patens* GTP binding protein

CC (GBP) full-length cDNA.

XX Sequence 667 BP; 169 A; 142 C; 185 G; 171 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 667; DB 13; Length 667;

XX Best Local Similarity 100.0%; Pred. No. 4.1e-220;

XX Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCCCGGAGTCGATGATACCAAGGCTGTGATCATGTTCTTGTAGATTGGTTTACGGCT 60

Db 1 ATCCCGGAGTCGATGATACCAAGGCTGTGATCATGTTCTTGTAGATTGGTTTACGGCT 60

QY 61 TTCTTGGAGCATAGGGCTGTGGAGAGAGGCAAAATCTGTTCTGGGTTCTGACA 120

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DB 181 CAACGCAATATCCAAAGTCAAGAGAGTGAATATCAACAGATGAAGTTCAAGCATTCG 240
QY 241 ATCTGGTGGCCCAACATTCGCTCGACGCGTGTGAGAGGACTCTATTCCTAAGTGGATG 300
DB 241 ATCTGGTGGCCCAACATTCGCTCGACGCGTGTGAGAGGACTCTATTCCTAAGTGGATG 300
QY 301 CATATAGTATCTCGTCAAGCAGTGAACAGGAGGATTTGCTGATCAAGAAAGAGC 360
DB 301 CATATAGTATCTCGTCAAGCAGTGAACAGGAGGATTTGCTGATCAAGAAAGAGC 360
QY 361 TCGATTCTCTTCTCTCGACGATTCCTGCTCCAGATTCCTGCTCTGCGGAAAC 420
DB 361 TCGATTCTCTTCTCTCGACGATTCCTGCTCCAGATTCCTGCTCTGCGGAAAC 420
QY 421 AGATTGATATCCCGTACGCTTCTTGTGAAGAGAGTTGGGTTCACTTGGGTTGACCA 480
DB 421 AGATTGATATCCCGTACGCTTCTTGTGAAGAGAGTTGGGTTCACTTGGGTTGACCA 480
QY 481 TGAACCTGGTAAGAGACGCTGACCTGGAGATGACCAATTCGGCCCATTTAGGTTT 540
DB 481 TGAACCTGGTAAGAGACGCTGACCTGGAGATGACCAATTCGGCCCATTTAGGTTT 540
QY 541 TCATGTGCAATATTTGCGCAAAATGGGGTACCGGTGAAGGTTTCAAGTGGATGCCAGT 600
DB 541 TCATGTGCAATATTTGCGCAAAATGGGGTACCGGTGAAGGTTTCAAGTGGATGCCAGT 600
QY 601 ACATCAAGTATGTTTCTCTGTGAAGAGAACTTAGCTCGGTGTTTAAAGCGAGAG 660
DB 601 ACATCAAGTATGTTTCTCTGTGAAGAGAACTTAGCTCGGTGTTTAAAGCGAGAG 660
QY 661 TTAAGC 667
DB 661 TTAAGC 667
```

RESULT 3

ABN89809/c
ID ABN89809 standard; cDNA; 805 BP.

AC ABN89809;

DT 18-SEP-2002 (first entry)

DE Physcomitrella patens GBP-1 partial cDNA sequence SEQ ID NO:1.

XX Physcomitrella patens; GBP; GTP binding protein; GBSRP; plant;
KM GTP binding stress-related protein; transgenic plant; agricultural;
KW environmental stress; salinity; drought; temperature; gene; se.

OS Physcomitrella patens.

PN US2002066124-A1.

PD 30-MAY-2002.

PF 06-APR-2001; 2001US-00828310.

PR 07-APR-2000; 2000US-0196001P.

PA (SIIV/) SIIVA O D C E.

PA (BOHN/) BOHNERT H J.

PA (THIE/) THIESEN N V.

PA (CHEN/) CHEN R.

PI Silva ODCE, Bohnert HJ, Thiesen NV, Chen R;
XX WPI, 2002-556781/59.

```
XX Novel GTP binding stress-related proteins and genes encoding the  
PT protein, useful for producing transgenic plants having increased  
PT tolerance to environmental stress as compared to wild type variety of  
PT plant cell.  
XX  
XX Example 5; Fig 1A; 73P; English.  
XX  
CC The present invention describes an isolated GTP binding stress-related  
CC protein (GBSRP) (I) from Physcomitrella patens, selected from GTP binding  
CC protein-1 (GBP-1), GBP-2, GBP-3, GBP-4 and GBP-5, or its orthologues. (I)  
CC can be used for producing a transgenic plant (e.g. maize, wheat, rice,  
CC oat, criticalale, rice, barley, soybean, peanut, cotton, rapeseed, canola,  
CC manhot, pepper, sunflower, tagetes, solanaceous plants, potato, tobacco,  
CC eggplant, tomato, Vicia species, pea, alfalfa, coffee, cacao, tea, Salix  
CC species, oil palm, coconut, perennial grass and forage crops). The  
CC transgenic plants produced have increased tolerance to environmental  
CC stresses (e.g. salinity, drought and temperature) as compared to a wild  
CC type variety of the plant, from the plant cell. GBSRP polynucleotide  
CC sequences can be used as markers for specific regions of the genome, and  
CC also in functional studies of P. patens proteins. They can also be used  
CC for evolutionary and protein structural studies. The present sequence  
CC represents a P. patens GBP-1 partial cDNA sequence, which is used in the  
CC exemplification of the present invention  
XX  
SO Sequence 805 BP; 214 A; 218 C; 161 G; 212 T; 0 U; 0 Other;  
Query Match 98.2%; Score 655; DB 6; Length 805;  
Best Local Similarity 100.0%; Pred. No. 6; 6e-216;  
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 CCGGTCCGTAAGTACCAAGGCTGTGACATGTTCTCTTGAATGGTTTAAAGCTTTCT 64  
DB 781 CCGGTCCGTAAGTACCAAGGCTGTGACATGTTCTCTTGAATGGTTTAAAGCTTTCT 722  
QY 65 TGGCAGCATATGGGCTGTGACAGAGGAGCCAAATCTGTTTCTGGGCTTCGACATGC 124  
DB 721 TGGCAGCATATGGGCTGTGACAGAGGAGCCAAATCTGTTTCTGGGCTTCGACATGC 662  
QY 125 TGGCAAGACTACTCTTCTGCAATGCTCAAGATGAGAACTGGGGCAATCAACCAAC 184  
DB 661 TGGCAAGACTACTCTTCTGCAATGCTCAAGATGAGAACTGGGGCAATCAACCAAC 602  
QY 185 GCAGTATCCAGCTGAGAGAGTGTGATCAACAGATGAAGTTCAAGCATTCGATCT 244  
DB 601 GCAGTATCCAGCTGAGAGAGTGTGATCAACAGATGAAGTTCAAGCATTCGATCT 542  
QY 245 GGGTGGCCACACATGCTCGACGCGTGTGAGAGGACTACTATGCTAAGTGGATGCTAT 304  
DB 541 GGGTGGCCACACATGCTCGACGCGTGTGAGAGGACTACTATGCTAAGTGGATGCTAT 482  
QY 305 AGTATATCTGCTGACGACAGTAGACAGGAGAGATTTGCTAGTCAAGAAAGACTCGA 364  
DB 481 AGTATATCTGCTGACGACAGTAGACAGGAGAGATTTGCTAGTCAAGAAAGACTCGA 422  
QY 365 TTCTCTTCTCTCGAAGATTTCTGTCCCAAGTTCTGTGCTGCTCGGGAACAAGAT 424  
DB 421 TTCTCTTCTCTCGAAGATTTCTGTCCCAAGTTCTGTGCTGCTCGGGAACAAGAT 362  
QY 425 TGAATCCGTAAGCTTTCTTCTGAAGAGAGTGGGTTTCAACTTGGTGGACATGAC 484  
DB 361 TGAATCCGTAAGCTTTCTTCTGAAGAGAGTGGGTTTCAACTTGGTGGACATGAC 302  
QY 485 CACTGTAAAGAACGCTGAACCTGGAGATGACCAATTCGGCCCATTTAGGTTTCAT 544  
DB 301 CACTGTAAAGAACGCTGAACCTGGAGATGACCAATTCGGCCCATTTAGGTTTCAT 242  
QY 545 GTGCAATATTTGGCGAAATGGGGTACAGTGAAGTTTCAAGTGAAGCCAGTACAT 604  
DB 241 GTGCAATATTTGGCGAAATGGGGTACAGTGAAGTTTCAAGTGAAGCCAGTACAT 182  
QY 605 CAAGTATGTTTCTCTGTAAGAGAGAACTTAGCTCGGTGTTTAAAGCGACGA 659
```



```
Db      181 CAAAGTATTGTTTCTCTGTGAAAAGAGAACTTAGCTCGGTGTTTAAGAGCGACGA 127

RESULT 4
ADT91564/c
ID      ADT91564 standard; cDNA; 805 BP.
XX
XX      ADT91564;
AC
XX      16-DEC-2004 (first entry)
DT
XX
XX      Physcomitrella patens GBSRP EST (expression sequence tag) partial cDNA.
DE
XX
XX      GTP-binding stress-related protein; GBSRP; transgenic plant;
KM      environmental stress tolerance; stress resistance; cell metabolism; EST;
KM      expression sequence tag; ss.
XX
XX      Physcomitrella patens.
OS
XX      US2004194163-A1.
PN
XX      30-SEP-2004.
PD
XX
XX      17-OCT-2003; 2003US-00688481.
PE
XX
XX      07-APR-2000; 2000US-0196001P.
PR      06-APR-2001; 2001US-00828310.
XX
XX      (BADI ) BASF PLANT SCI GMBH.
PA
XX
XX      Da Costa B Silveiro, Bohnert HJ, Thieleen NV, Chen R;
PI      WPI; 2004-698822/68.
DR
XX
XX      Novel isolated nucleic acid encoding polypeptide e.g., GTP-binding stress
PT      -related protein, useful for producing vector utilized for producing
PT      transgenic plant that has increased tolerance to environmental stress.
XX
XX      Example 5; SEQ ID NO 1; 622p; English.
XX
XX      The invention relates to nucleic acid sequences encoding GTP-binding
CC      stress-related protein (GBSRP). GBSRP DNA is useful for producing a
CC      recombinant expression vector utilized for producing a transgenic plant
CC      that has increased tolerance to environmental stress, for identifying
CC      Physcomitrella patens and related organisms, for identifying and
CC      localizing P. patens sequences of interest, for evolutionary studies, for
CC      determining GBSRP regions required for function, for modulating GBSRP
CC      activity, for modulating metabolism of one or more cell function, for
CC      modulating transport of one or more compounds, for modulating stress
CC      resistance or as markers for specific regions in the genome of P. patens.
CC      The present sequence is the Physcomitrella patens GBSRP EST (expression
CC      sequence tag) partial cDNA.
XX
XX      Sequence 805 BP; 214 A; 218 C; 161 G; 212 T; 0 U; 0 Other;
SQ

Query Match      98.2%; Score 655; DB 13; Length 805;
Best Local Similarity 100.0%; Pred. No. 6,6e-216;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CGGGTCGATGATCAAGAGCTGGTACCAATCTTCTTGATGATGTTTAAAGGCTTCT 64
Db      781 CGGGTCGATGATCAAGAGCTGGTACCAATCTTCTTGATGATGTTTAAAGGCTTCT 722
QY      65 TGCAGCATAGGCTGTGCGAAGAGAGGCCAAATCCGTTTCTGGGCTCGCAATGC 124
Db      721 TGCAGCATAGGCTGTGCGAAGAGAGGCCAAATCTCTGTTCTGGGCTCGCAATGC 662
QY      125 TGCAGCATAGCTTCTTCTGCAATGCTTCAAGATGAGAACTGGGGCAACATCAACCAAC 184
Db      661 TGCAGCATAGCTTCTTCTGCAATGCTTCAAGATGAGAACTGGGGCAACATCAACCAAC 602
QY      185 GCAATATCCAAAGCTCAGAGAGTTGATATCAACAGATGAAGTTCAAAGATTCGATCT 244
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Db      601 GCAATATCCAAAGCTCAGAGAGTTGATATCAACAGATGAAGTTCAAAGATTCGATCT 542
QY      245 GGGTGGCCACACAATCGCTCGACGCGTGTGAGAGGACTATATGCTAAGGTGATGCTAT 304
Db      541 GGGTGGCCACACAATCGCTCGACGCGTGTGAGAGGACTATATGCTAAGGTGATGCTAT 482
QY      305 AGGTATCTTCGTGAGACGAGTATACAGAGGAGAAATTTGCTGATCAAAAGAGCTCGA 364
Db      481 AGGTATCTTCGTGAGACGAGTATACAGAGGAGAAATTTGCTGATCAAAAGAGCTCGA 422
QY      365 TTCTCTTCTCTCCGACGATCTCTGTCCCAAGTTCCGTGCTGCTCGTGGGAAACAAGAT 424
Db      421 TTCTCTTCTCTCCGACGATCTCTGTCCCAAGTTCCGTGCTGCTCGTGGGAAACAAGAT 362
QY      425 TGATATCCGTAAGCTTCTTCTGAAAGACGATTCGGGTTCACACTTGAGTTGACCATGAC 484
Db      361 TGATATCCGTAAGCTTCTTCTGAAAGACGATTCGGGTTCACACTTGAGTTGACCATGAC 302
QY      485 CACTGTGTAAGGAACGGTGAACCTGGGAGATACCAACATTCGGCCCATTTAGGTTTTCAT 544
Db      301 CACTGTGTAAGGAACGGTGAACCTGGGAGATACCAACATTCGGCCCATTTAGGTTTTCAT 242
QY      545 GTGCAGTATTGTCGCAAAATGGGGTACCGGTGAAGGTTTCAAGTGAATGACCCAGTACAT 604
Db      241 GTGCAGTATTGTCGCAAAATGGGGTACCGGTGAAGGTTTCAAGTGAATGACCCAGTACAT 182
QY      605 CAAAGTATTGTTTCTCTGTGAAAGAGAACTTACCTCGGTGTTTAAAGCGACGA 659
Db      181 CAAAGTATTGTTTCTCTGTGAAAGAGAACTTACCTCGGTGTTTAAAGCGACGA 127

RESULT 5
ABK71577
ID      ABK71577 standard; cDNA; 928 BP.
XX
XX      ABK71577;
AC
XX      30-JUL-2002 (first entry)
DT
XX
XX      Human dlthp polynucleotide #43.
DE
XX
XX      Human; dlthp; diagnostic and therapeutic polynucleotide; gene; ss; bone;
KM      cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;
KM      inflammatory disorder; viral infection; bacterial infection; seizure;
KM      fungal infection; parasitic infections; developmental disorder; breast;
KM      endocrine disorder; metabolic disorder; neurological disorder; cervix;
KM      gastrointestinal disorder; transport disorder; gene therapy; kidney;
KM      adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
KM      skin; testis; thymus.
XX
XX      Homo sapiens.
OS
XX      WO200220754-A2.
PN
XX      14-MAR-2002.
PD
XX
XX      29-AUG-2001; 2001WO-US027127.
PF
XX
XX      05-SEP-2000; 2000US-0229747P.
PR      05-SEP-2000; 2000US-0229748P.
XX
XX      05-SEP-2000; 2000US-0229749P.
PR      05-SEP-2000; 2000US-0229750P.
XX
XX      05-SEP-2000; 2000US-0229751P.
PR      05-SEP-2000; 2000US-0230583P.
XX
XX      06-SEP-2000; 2000US-0230584P.
PR      06-SEP-2000; 2000US-0230514P.
XX
XX      06-SEP-2000; 2000US-0230515P.
PR      06-SEP-2000; 2000US-0230517P.
XX
XX      06-SEP-2000; 2000US-0230518P.
PR      06-SEP-2000; 2000US-0230519P.
XX
XX      06-SEP-2000; 2000US-0230595P.
PR      06-SEP-2000; 2000US-0230597P.
XX
XX      06-SEP-2000; 2000US-0230598P.
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PR 06-SEP-2000; 2000US-0230599P.
PR 06-SEP-2000; 2000US-0230610P.
PR 06-SEP-2000; 2000US-0230656P.
PR 06-SEP-2000; 2000US-0230988P.
PR 07-SEP-2000; 2000US-0230951P.
PR 07-SEP-2000; 2000US-0231163P.
PR 07-SEP-2000; 2000US-0231167P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Stuart J., Lincoln SE, Altue CM, Dufour GE, Chalup MS, Hillman JL,
PI Jones AL, Yu JY, Wright RU, Gietzen D, Liu TF, Yap PE, Dahl CR,
PI Momiyama MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM,
PI Gerstin EH, Peralta CH, David MH, Panzer SR, Flores V, Dafio A,
PI Marwaha R, Chen AJ, Chang SC, Au AP, Imman RR;
XX
XX WPI; 2002-383054/41.
DR P-PSDB; ABG59985.
XX
XX An isolated polynucleotide useful in diagnostics and therapeutics.
PT
PS Claim 1; Page 427; 686bp; English.
XX
XX The invention relates to human diagnostic and therapeutic (dthp)
CC polynucleotides and their associated polypeptides (DTHP polypeptides).
CC The sequences of the invention are used in the treatment and diagnosis of
CC cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
CC (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast,
CC cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or
CC thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,
CC psoriasis, osteoporosis), viral infections, bacterial infections, fungal
CC infections, parasitic infections, developmental disorders (e.g. anaemia,
CC epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),
CC endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders
CC (e.g. obesity, diabetes), neurological disorders (e.g. stroke,
CC amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal
CC disorders (e.g. ulcerative colitis, lysinuria) and transport disorders
CC (e.g. myotonic dystrophy, cataractia, peripheral neuropathy). Sequences
CC ABK71535-ABK71809 represent human dthp polynucleotides of the invention
XX
SQ Sequence 928 BP; 206 A; 251 C; 262 G; 209 T; 0 U; 0 Other;
Query Match 51.0%; Score 340.4; DB 6; Length 928;
Best Local Similarity 74.7%; Pred. No. 1e-106;
Matches 441; Conservative 0; Mismatches 146; Indels 3; Gaps 1;
QY 23 GGCTGTACCAGTTCTTGTAGATTGTTTACGGCTTCTTTCGAGCATAGAGGCTGTG 82
DB 153 GGTGGGGAGATGTTCTCTGGAGCTGTTCTACGGGGGTCTGGCCCTCGGCTGTG 212
QY 83 GCAGAAAGAGGCCAAATCTCTGTTTGGGCTTCGACATGCTGGCAAGACTTCTTCT 142
DB 213 GCAGAAAGAGGCCAAATCTCTTCTTCTGCTTCGACAGCCGCGAAGCCAGCTGTCT 272
QY 143 GCACATGCTCAAGATAGAGAAACGCGGCAACATCAACCAAGCATCAAGCTCAGA 202
DB 273 CCACATGCTCAAGAGACGAGCGGTTGTGACGACACCCAGCAGCAGCTGCGA 332
QY 203 GGAATTGATATCAACAGATGTAAGTTCAAGATTCGATCGGTGGCCACAATTCGC 262
DB 333 GGAATCAGATCGGCAAGATCAAGTTCAAGGCTTGAACCTCGGGGCGCACAGATCGC 392
QY 263 TCACACCGGTGTGAGGAGCTACTATGTAAAGTGTGATGTATTTCTCGACGC 332
DB 393 GCCCGCGGTGTGAAAGATTACTACGCAAGGTGTGATGCTGTATTAACCTGTAGATGC 452
QY 323 AGTAGACAGGAGGATTTGCTGAGTCAAGAAAGAGCTGATTTCTTCTCCGACGA 382
DB 453 ATATGATTAAGAGCGATTTGCTGATTAAGAAAGAGCTGAGTCTCTCTGTATGA 512
QY 383 TTCTGTGTCCCAAGTTCTGTGCTGTCTGTGGGAAACAGATGATATCCCGTAGCTTC 442
DB 513 TTCTTTGGCCAAATGTTCTATTTCTCATCTTGGCAACAAATTTGATATCCATATGCTGC 572

QY 443 TTCTGAAGACGAGTTCCGTTTCACTTGGTTTGACCA---TGACCATCTGTAAAGAAC 499
DB 573 CTCTGAAGAGGAGCTACAGCTATACCTTAGCCCTTGGACACTTCACAAACGGGAAGGCAA 632
QY 500 GGTGAACCTGGAGATATGACATTTGCGCCATTTGAGTTTTCATGTGCAATTTGTGCG 559
DB 633 GGTCAACCTTGGCGGCTCAATGTCCTTCACTTGAAGGCTTTCATATGTGCAAGTTGTCG 692
QY 560 CAAATGGGTACGGTGAAGTTTCAAGTGAATGACCCAGTACATCAAGT 609
DB 693 CAAGATGGGCTACGGTATGTTTCAAGTGGGTCTTCCAGTACATCAAGT 742
RESULT 6
ADX12667
ID ADX12667 standard; cDNA; 998 BP.
XX
XX ADX12667;
AC
XX
XX 21-APR-2005 (first entry)
DT
XX
XX Plant full length insert polynucleotide seqid 7242.
DE
XX
XX Plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomanan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
XX Unidentified.
OS
XX
XX US2004034888-A1.
PN
XX
XX 19-FEB-2004.
PD
XX
XX 28-APR-2003; 2003US-00425114.
PF
XX
XX 06-MAY-1999; 99US-00304517.
PR
XX
XX 05-NOV-2001; 2001US-00985678.
PR
XX
XX (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TAB/) TABASKA J E.
PA (CAOV/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
XX WPI; 2004-180133/17.
DR
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
PT
XX
PS Claim 1; SEQ ID NO 7242; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomanan,
CC lignin or plant growth regulators, for increasing the rate of homologous

DB 324 TCCGCCGCCGCTCTGGAAGAGTACTACGCCAAGGTGATGCTGTGTACTTGATG 383
QY 319 AGCAGTGAAGCAGAGGAGATTTGCTGAGTCAGAAAGAGCTCGATTCCTCTCCG 378
DB 384 ATGCTGTGCAAGGAACGTTTGGCGAGTCGAAGAGGAGCTCGATGCGCTTCTGCA 443
QY 379 ACAGATTCCTGTCCTCCAGTTCTCTGCTGCTCCCTGGGAAACAGATTTGATTCCTG 438
DB 444 ATGACTCCCTGGAACGTTCTCTTCTCTCACTATGCGGCAACAGATTTGATTCCTG 503
QY 439 CTTCTTCTGAAGCAGAGTTCGCTTCACTTGGGTTGACCA--TGACCCTGTGAAG 495
DB 504 CGGCTTCAGAGGAGAGCTGAGGTAAGTACTCTCGCTGAGCACTTCACAAACCGGGA 563
QY 496 GAACGCTGAACCTGGAGATAGCAACATTCGCGCCATTTGAGTTTCATGTGAGTATG 555
DB 564 GCAACGTGAACCTGGAGTCCAGCTCCAGCTCCGCCCCCTGGAGATCTTCATGTGAGT 623
QY 556 TCGCGAAATGGGGTACGCTGAGAGTTTCAAGTGAAGCCAGTACATCAAGTATG 613
DB 624 TCGCAAGATGGGCTATGGCGAAGGCTTCAATGATGTCTCAATCAATCAAGTATG 681
RESULT 8
AD30716
ID ADX30716 standard; cDNA; 966 BP.
XX
AC ADX30716;
XX
DT 21-APR-2005 (first entry)
XX
DE plant full length insert polynucleotide seqid 13536.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
OS unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
XX
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIU/J) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D. K.
PA (SCRE/) SCREEN S. E.
PA (TABAS/) TABASKA J. E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
XX WPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 13536; 15bp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence

CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 966 BP; 225 A; 218 C; 294 G; 229 T; 0 U; 0 Other;
XX
Query Match 49.8%; Score 332.4; DB 13; Length 966;
Best Local Similarity 73.4%; Pred. No. 6,3e-104;
Matches 439; Conservative 0; Mismatches 156; Indels 3; Gaps 1;
QY 19 CCAAGGCTGTGACCAATGTTCTTGTAGATGATGCTTTTACCGCTTCTTGGAGCATAGGC 78
DB 116 CCGAGTTGTAAAGATGTTCTGTGTGACTGGTTATGAGGAGTGTGCGCTTGCGC 175
QY 79 TGTGGCAAGAGAGGCAAAATCTGTTCTTGTGGGTTCGACAATGCTGGCAAGACTATC 138
DB 176 TGTGGCAAGAGAGGCTAATGATCTCTTCTTGGCTTCACAAACGCGGCAAGACACC 235
QY 139 TTTGTGACATGCTCAAGATGAGAAACCTGGGCAACATGACCAACGAGTATCAACGT 198
DB 236 TCTCTCAATGCTGAAGAGAGAGCGGCTGTACAGCACGCGAGCATACCCACGT 295
QY 199 CAGAGAGTTGATATCAACAGAGTGAAGTTCAAGACATTCATCTGAGTGGCCACACA 258
DB 296 CAGAAGAGTTGAGCATTCGACAGAGTCAAGTCAAGCGTTTCACTTGGGGGCGACAGA 355
QY 259 TCGCTGACGCGGTGTGAGGAGTACTATGCTAAGTGAATGCTATAGTATCTGCTG 318
DB 356 TCGCCCGCGCGCTGTGGAAGAGTACTACGCCAAGGTATGCTGTGTACTTGCTG 415
QY 319 AGCAGTGAACAGGAGAGATTTGCTGAGTCAAGAAAGAGCTCGATTCCTCTCCG 378
DB 416 ATGCTGTGAACAAGAACGTTTTCGAGTCCAGAGTCAAGAGAGCTTGATGCGCTTCTG 475
QY 379 ACAGATTCCTGTCCTCCAGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 438
DB 476 ATGACTCCCTTGAAGAGTCTCTTCTCTCACTATGCGGCAACAAGATTTGATTCCTG 535
QY 439 CTTCTTCTGAAGCAGAGTTCGCTTCACTTGGGTTGACCA--TGACCCTGTGAAG 495
DB 536 CGGCTTCAGAGAGAGAGCTGAGGTAAGTACTCGGCTGAGCAACTTCACAAACCGGGA 595
QY 496 GAACGCTGAACCTGGAGATAGCAACATTCGCGCCATTGAGTTTCATGTGAGTATG 555
DB 596 GCAACGTGAACCTGGAGAGTCCAGTCCAGTCCGCGCTTGAAGATCTTCATGTGAGT 655
QY 556 TCGCGAAATGGGGTACGCTGAGAGTTTCAAGTGAAGCCAGTACATCAAGTATG 613
DB 656 TCGCAAGATGGGCTATGGCGAAGGCTTCAATGATGTCTCAATCAATCAAGTATG 713
RESULT 9
AD30716
ID ADX62537 standard; cDNA; 1017 BP.
XX
AC ADX62537;
XX
DT 21-APR-2005 (first entry)
XX
DE plant full length insert polynucleotide seqid 33380.

XX plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
XX
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D. K.
PA (SCREEN S E.) SCREEN S. E.
PA (TABASKA J E.) TABASKA J. E.
PA (CAOY/) CAO Y.
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 33380; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
XX Sequence 1017 BP; 229 A; 229 C; 311 G; 248 T; 0 U; 0 Other;
SQ

Query Match 49.8%; Score 332.4; DB 13; Length 1017;
Best Local Similarity 73.4%; Pred. No. 6.5e-104;
Matches 439; Conservative 0; Mismatches 156; Indels 3; Gaps 1;
QY 19 CCAAGCTGTGATCCATGTTCTTGAATGCTTTTACGGCTTCTTGCGAGCATAGGGC 78
DB 97 CCGAGGTGTAAAGATGTTCTGTGTGACTGTCTTATGAGGCTCTGACATCGCTTGGGC 156
QY 79 TGTGCGAAGAGAGAGCCAAATCTGTTCTGGGCTCTGCAATGCTGCAAGACTATC 138
DB 157 TGTGCGAAGAGAGAGCTAAGATCTCTTCTGCTTGGCTTGAAGAGCCGGCAAGCACCC 216
QY 139 TTTCGACATGCTCAAGAGTGAAGAACTGGGGCAACATCAACCAACGATATCCAACT 198

DB 217 TCCCTACATGCTGAAGAGCGAGCGGCTCTTACAGACCAAGCCAGCGATACCCACGT 276
QY 199 CAGAGAGTTGATATCAACAGATGAGATTCAAGACATTCGATCTGGGTGGCCACACA 258
DB 277 CAGAAAGTTGAGCATTGCGACAGATCAAGTTCAAGCGTTTGCACCTTGGGGGGCCACACA 336
QY 259 TCGCTGACGCGGTGTGAGAGGACTACTATGCTAAGGTGATGTATAGTATCTGTGTG 318
DB 337 TCGCCCGCGCGCTGTGAAGGACTACTACGCCAAGGTATGTGTGTGTACTTGTGTG 396
QY 319 ACGGCTAGACAGAGGAGATTTGCTGAGTCAAGAAAGAGCTCGATTCTTCTCTCCG 378
DB 397 ATGCTGTGACAGAGAACGTTTGGCCGAGTCGAGAGAGAGGCTTGATGGGCTTCTTGCAG 456
QY 379 ACGATTCTGTCCCAAGTTTCTGTGCTGCTGCTGCGAACAAGATTGATATCCCGTAGC 438
DB 457 ATGACTCCCTTGAAGACGTTTCTTCTCTATCTGAGCAACAAGATTGACATCCATAG 516
QY 439 CTTCTTCTGAAGACGATGCGGTTCAACTTGGGTTGACCA--TGACCACTGTAAAG 495
DB 517 CCGCTTCAAGAGAGAGCTGAGGTACTACCTCGGCTGAGCACTTCAACCCGGGAAAG 576
QY 496 GAAAGGTGAACCTGGGAGATAGCAATTCGGGCCATTGAGGTTTCATGTGAGATTG 555
DB 577 GCAACGTGAACCTGGCCGACTCCAAATGTCGGGCCCTGAGAGATCTTCAATGAGTGTG 636
QY 556 TGGCAAAATGGGGTACGGGTGAAGTTTCAAGTGATGACCCAGTACATCAAGTATT 613
DB 637 TGGCAAGATGGGCTATGGCGAAGGCTTCAAAATGATGTCTGATCATCAAGTGTAGT 694

RESULT 10
ADM45502
ID ADM45502 standard; DNA; 811 BP.
XX
XX ADM45502;
XX
XX 03-JUN-2004 (first entry)
XX
XX Insect resistance associated DNA sequence SeqID909.
XX
XX Insect resistant phenotype; plant protectant; gene therapy;
KW Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;
KW Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.
XX
XX Unidentified.
XX
XX NC2003020025-A2.
XX
XX 13-MAR-2003.
XX
XX 30-AUG-2002; 2002MO-US027882.
XX
XX 31-AUG-2001; 2001US-0316319P.
XX
XX (DOWC) DOW CHEM CO.
XX
XX Shukla V, Meade T, Larrinua I;
XX
XX WPI; 2003-290133/28.
XX
XX New isolated nucleic acid having expression that results in an insect
PT resistant phenotype, useful for conferring insect resistance and for
PT producing insect-resistant plants.
XX
XX Claim 1; SEQ ID NO 909; 396pp; English.
XX
XX This invention relates to a novel isolated nucleic acid comprising, or
CC hybridising under low stringent conditions to, any of the 1214 nucleic
CC acid sequences given in the specification, where the expression of the
CC nucleic acid in a plant results in an insect resistant phenotype. The
CC invention may be useful as a plant protectant or for gene therapy. The

CC genes are derived from Arabidopsis thaliana, Nicotiana benthamiana, Oryza
CC sativa and Papaver rhoeas. The isolated nucleic acid and vector are
CC useful for conferring insect resistance and for producing insect-
CC resistant plants. The present sequence is that of a DNA sequence of the
CC invention which may confer insect resistance to plants.

XX
SQ Sequence 811 BP; 219 A; 157 C; 199 G; 236 T; 0 U; 0 Other;

Query Match 49.7%; Score 331.2; DB 11; Length 811;
Best Local Similarity 73.6%; Pred. No. 1,5e-103;

Matches 436; Conservative 0; Mismatches 153; Indels 3; Gaps 1;

```

Oy 28 GTACCAATGTTCTTGTAGATTTGTTTACGGCTTTCTGGACATAGGGCTGTGACAGA 87
Db 126 GCAAGATGTTCTTGTAGATTTGTTTCTATGAAATTTCTAGCAAGCTTGGATTATGGCAGA 185
Oy 88 AGGAGGCCAAATCTGTTCTGCTGCTGACATGCTGCAAGACTCTTCTGCACA 147
Db 186 AGGAGGCTAAGATCTGTTTGGGCTCGATATGCGCAAAACCACTTACTCATTA 245
Oy 148 TGCTCAAGATGAGAACTGGGCAACATACCAACGCGATTTCCAGCTCAGAGAGT 207
Db 246 TGTGAAAGATGAGATTTGTTCAATCAGCAACAAATATCCGACCTCAGAGAGC 305
Oy 208 TGAGTATCAACAGATGAAGTTCAAGCATTCGATCGGTGGCCACAAATGCTCGAC 267
Db 306 TTAGTATCGGCAAGATCAAGATTCGAATTTGCTGGGTGATCAATATGCTGACC 365
Oy 268 GCGTGTGAGGAGTACTATGCTAAGTGTGATCTATGATATCTGTCGACGACAGTAC 327
Db 366 GTGTTTGAAAGATTTATATGCTAAGTGTGATGCTGTGTATATCTTGATTTCTTTG 425
Oy 328 ACAGGAGAGATTTGCTGAGTCAAGAAAGAGCTCGATTTCTTCTCTCCAGAGATTC 387
Db 426 ACAAGAGAGATTTGCAAGATTCAGAAAGAGCTGTGATCTCTCTGAGAGAGTCT 485
Oy 388 TGTCCCAAGTCTGCTGCTGCTGCTGGAAGAAAGATGATTCCTGCTGCTCTTCTG 447
Db 486 TGGCAACTGTTCTTCTCTCTATCTGAGTTACAGATAGCATTCCTCATGCTGCTCAG 545
Oy 448 AAGACGAGTTCGCTTCACTTGGTTGAC---CATGACACTGTGTAAGAACGCTGA 504
Db 546 AAGATGAACTGCGTTACATATGGGGCTAACGGGCGTCACTGCGAAAGGAAAGTAA 605
Oy 505 ACCTGGAGATAGCAACATTCGCGCCATTGAGGTTTTCATGTGCAATTTGTGGCAAAA 564
Db 606 ACCTGGCAGATTCCTCAATGTCGCTCAGTTGAGGATATTCATGTGCAAGTATGTCGCAAAA 665
Oy 565 TGGGGTACGCTGAAGTTTCAAGTGTATGACCAAGTACATCAATGATTTGTT 616
Db 666 TGGGATATGAGAAAGCTTCAGATGATGATCTCAGATATATCAAGTAAATTTGTT 717
```

RESULT 11

ID ADM45760 standard; DNA; 830 BP.

XX ADM45760;

XX 03-JUN-2004 (first entry)

XX Insect resistance associated DNA sequence SegID1167.

XX Insect resistant phenotype; plant protectant; gene therapy;

XX Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;

XX Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.

XX Unidentified.

XX WO2003020025-A2.

XX 13-MAR-2003.

PF 30-AUG-2002; 2002WO-US027882.
XX
PR 31-AUG-2001; 2001US-0316319P.

XX (DOWC) DOW CHEM CO.

XX Shukla V, Meade T, Larrinua I;

XX MPI; 2003-290133/28.

XX New isolated nucleic acid having expression that results in an insect
XX resistant phenotype, useful for conferring insect resistance and for
XX producing insect-resistant plants.

XX Claim 1; SEQ ID NO 1167; 396bp; English.

XX This invention relates to a novel isolated nucleic acid comprising, or
XX hybridizing under low stringent conditions to, any of the 1214 nucleic
XX acid sequences given in the specification, where the expression of the
XX nucleic acid in a plant results in an insect resistant phenotype. The
XX invention may be useful as a plant protectant or for gene therapy. The
XX genes are derived from Arabidopsis thaliana, Nicotiana benthamiana, Oryza
XX sativa and Papaver rhoeas. The isolated nucleic acid and vector are
XX useful for conferring insect resistance and for producing insect-
XX resistant plants. The present sequence is that of a DNA sequence of the
XX invention which may confer insect resistance to plants.

XX Sequence 830 BP; 221 A; 165 C; 204 G; 240 T; 0 U; 0 Other;

Query Match 49.7%; Score 331.2; DB 11; Length 830;
Best Local Similarity 73.6%; Pred. No. 1,5e-103;

Matches 436; Conservative 0; Mismatches 153; Indels 3; Gaps 1;

```

Oy 28 GTACCAATGTTCTTGTAGATTTGTTTACGGCTTTCTGGACATAGGGCTGTGACAGA 87
Db 145 GCAAGATGTTCTTGTAGATTTGTTTCTATGAAATTTCTAGCAAGCTTGGATTATGGCAGA 204
Oy 88 AGGAGGCCAAATCCGTTTCTGCTGCTGACAAATGCTGCAAGACTCTTCTGCACA 147
Db 205 AGGAGGCTAAGATCTGTTTGGGCTCGATATGCGCAAAACCACTTACTCATTA 264
Oy 148 TGCTCAAGATGAGAACTGGGCAACATCAACGAGATTCACAGCTCAGAGAGT 207
Db 265 TGTGAAAGATGAGATTTGTTCAACATCAGCAACAAATATCCGACGTCAGAGAGC 324
Oy 208 TGAATATCAACAGATGAAGTTCAAAAGATTCGATTCGCTGCGCAACAAATGCTCGAC 267
Db 325 TTAGTATCGGCAAGATCAAGTTCAAAGCATTTGATCTTGAGTGTCAATTAATGCTCGCC 384
Oy 268 GCGTGTGAGGAGTACTATGCTAAGTGTGATCTATGATATCTGTCGACGACAGTAC 327
Db 385 TGTGTTTGAAAGATTTATATGCTAAGTGTGATGCTGTTGATATCTTGAGTATTTCTTTG 444
Oy 328 ACAGGAGAGATTTGCTGAGTCAAGAAAGAGCTGATTTCTTCTCGACGATTTCTC 387
Db 445 ACAAGAGAGATTTGCAAGATTCAGAAAGAGCTGATGCTGCTCTGACAGATCTT 504
Oy 388 TGTCCCAAGTCTGCTGCTGCTGCTGGAAGAAAGATGATTCCTGCTTCTTCTG 447
Db 505 TGGCAACTGTTCTTCTCTCTATCTGAGTTACAGATAGCATTCCTCATGCTGCTCAG 564
Oy 448 AAGACGAGTTCGCTTCACTTGGTTGAC---CATGACACTGTGTAAGAACGCTGA 504
Db 565 AAGATGAACTGCGTTACATATGGGGCTAACGGGCGTCACTGCGAAAGGAAAGTAA 624
Oy 505 ACCTGGAGATAGCAACATTCGCGCCATTGAGGTTTTCATGTGCAATTTGTGGCAAAA 564
Db 625 ACCTGGCAGATTCCTCAATGTCGCTCAGTTGAGGATATTCATGTGCAAGTATGTCGCAAAA 684
Oy 565 TGGGGTACGCTGAAGTTTCAAGTGTATGACCAAGTACATCAATGATTTGTT 616
Db 685 TGGGATATGAGAAAGCTTCAGATGATGATCTCAGATATATCAAGTAAATTTGTT 736
```


RESULT 12
AEB67368
ID AEB67368 standard; DNA; 952 BP.
AC AEB67368;
XX
DT 22-SEP-2005 (first entry)
XX
XX Rice genome derived DNA sequence, SEQ ID 2513.
DE
XX transcription; gene regulation; transgenic plant; RNA interference;
KM transformation; antibody; ds.
XX
XX Oryza sp.
XX JP2005185101-A.
PN 14-JUL-2005.
XX
XX 11-DEC-2002; 2002JP-00383870.
PF
XX 30-MAY-2002; 2002JP-00203269.
PR
XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
PA (SEIB-) SEIBUTSUKAI TOKUTEI SANGYO GIJUTSU.
PA (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.
PA (KOKU-) ZH KOKUSAI KAGAKU SHINKO ZAIDAN.
XX
PI Kikuchi H, Hayashizaki Y, Otsomo Y, Matsubara K, Murakami K,
PI Kishimoto N, Seto K, Nagata T, Kawakami N, Yazaki U, Ishikawa M,
PI Doi K, Kawai U;
XX WPI; 2005-566181/58.
XX
XX Novel DNA encoding transcription factor, derived from rice plant, useful
PT for obtaining transcriptional-regulatory regions in plant and for
PT producing modified plant.
XX
PS Claim 1; SEQ ID NO 2513; 2928bp; Japanese.
XX
XX The invention relates to a novel DNA sequence encoding a transcription
CC factor derived from a plant. The invention further comprises antisense
CC RNA sequences, ribozyme activity RNA, RNAi sequences, a vector,
CC transformed plant cells, antibodies and proteins, all related to the
CC novel plant DNA sequences of the invention. The novel DNA is preferably
CC derived from a rice-genome database. The invention further provides a
CC method for determining the transcription regulatory regions of the rice
CC genome. The novel DNA is useful for controlling the expression of a gene
CC in a plant and for producing a modified plant with desired and different
CC characteristics. The plant DNA and method enables the acquisition of many
CC transcriptional-regulatory regions. This polynucleotide represents a DNA
CC sequence taken from a rice genome clone library for use in the invention.
CC Note: This sequence is not shown in the specification. It has been
CC retrieved from a sequence listing in electronic format from the Japanese
CC Patent Office. The invention claims DNA sequences of SEQ ID Nos 1 to
CC 28469 and encoded protein sequences of SEQ ID Nos 28470 to 56791,
CC however, the sequence listing only provided the DNA sequences of SEQ ID
CC Nos 1 to 3032.
XX
XX Sequence 952 BP; 209 A; 248 C; 272 G; 223 T; 0 U; 0 Other;
SQ
Query Match 49.5%; Score 330.4; DB 14; Length 952;
Best Local Similarity 74.3%; Pred. No. 3,1e-103;
Matches 431; Conservative 0; Mismatches 146; Indels 3; Gaps 1;
QY 33 ATGTTCTTGTAGATTGCTTTTACGCTTTCTTCGACATAGGCTGTGACAGAGAG 92
DB 130 ATGTTCTGTTGAGCTGCTCTACGCGGCTGCTGCGCTGCGGCTGTGACAGAGAG 189
QY 93 GCCAAATCCGTTCTGCGCTGCGACAAATGCTGCAAGATCTCTTTCGACATGTC 152
DB 190 GCCAAGATCTCTCTCTGCGCTGCGACAAAGCGGCAAGACCAAGCTCTCCACATGTC 249

QY 153 AAGATGAGAAATGGGGCAACATCAACCAACCAAGTATCCAAAGTTCAGAGAGTTGACT 212
DB 250 AAGACGAGAGATTGGTGGAGCATCAACCTACCAAGTATCCGCTTCTGAAGAGCTGAGC 309
QY 213 ATCAACAGATGAGTTCAAGATTCGATCTGGGTGGCCACACATTCGCTGACGGGTG 272
DB 310 ATTGGGAAGATCAAGTTCAAGGCGTTGATTTTGAAGAGCCATCAATTTGCTCCCGTGTG 369
QY 273 TGAAGGACTACTATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 332
DB 370 TGAAGAGACTACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 429
QY 333 GAGAGATTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 392
DB 430 GAGAGGTTCTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 489
QY 393 CAAGTTCCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 452
DB 490 ACCGTCCTTCTGATCTGAGGCAACAGATGATGATGATGATGATGATGATGATGATGATG 549
QY 453 GAGTTCGCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 509
DB 550 GAGTTCGCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 609
QY 510 GAGATGACAAATTCGCGCCCATTTGAGTTGATGATGATGATGATGATGATGATGATGATG 569
DB 610 GCGAGATGCAACGTTGCGCCCATTTGAGTTGATGATGATGATGATGATGATGATGATGATG 669
QY 570 TAGGTTGAAGGTTTCAAGTGGATGATGATGATGATGATGATGATGATGATGATGATG 609
DB 670 TAGGTTGAAGGTTTCAAGTGGATGATGATGATGATGATGATGATGATGATGATGATG 709
RESULT 13
ADX45605
ID ADX45605 standard; cDNA; 986 BP.
XX
XX ADX45605;
XX
DT 21-APR-2005 (first entry)
XX
XX Plant full length insert polynucleotide seqid 20145.
DE
XX plant protectant; plant growth regulator; gene therapy; plant;
KM recombinant DNA construct; physical array; plant breeding marker;
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KM extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KM galactomannan production; lignin production; plant growth regulator;
KM yield; plant growth; plant development; seed oil; protein yield;
KM protein content; gene; ss.
XX
XX Unidentified.
OS
XX US2004034888-A1.
PN
XX 19-FEB-2004.
PD
XX 28-APR-2003; 2003US-00425114.
PF
XX 06-MAY-1999; 99US-00304517.
PR
XX 05-NOV-2001; 2001US-00985678.
XX
XX (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAS/) TABASKA J E.
PA (CAO/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
PI


```
Matches 431; Conservative 0; Mismatches 146; Indels 3; Gaps 1;
Qy 33 ATGTTCTTGTAGATGGTTTAAAGCGCTTCTTSCGAGCATAGGGCTGTGGCAAGAG 92
Db 155 ATGTTCTTGTAGATGGTTTAAAGCGGTGTGGCTTCTTSCGAGCATAGGGCTGTGGCAAGAG 214
Qy 93 GCCAAAATCTGTTTCTGGGTCTCGACAAATGCTGGCAAGACTCTTCTGACATGCTC 152
Db 215 GCGAAGATCTCTTCTCTGCGCTCGACAAACGCGCAAGACACGCTGCTCCATGCTC 274
Qy 153 AAGGATGAGAAACCTGGGCAACATCAACCAACGAGATCAAGATCAAGAGAGTTAGT 212
Db 275 AAGGACGAGCGGTGTGGCAACGACCGACGACGACCGAGCTGGAGAGCTGAC 334
Qy 213 ATCAACAGATGAGATTCAAGCATTTGATCTGGGTGGCCACACAAATGCTCGACGGCTG 272
Db 335 ATCCGCAAGATCAAGATTCAAGGCTTTCGACTCGGCGGCAACGATTCGCGCGGCTC 394
Qy 273 TGGAGGACTACTATGCTAAGTGTGATGCTATGATCTGTCGACGCAAGTACAGAG 332
Db 395 TGGAGGATTTACTACGCAAGATGATGCTGATATACCTGATGATGCTGATGATG 454
Qy 333 GAGGATTTGCTGATGCAAAAGAGCTGATTTCTTCTCTCCGACGATCTCTGCTCC 392
Db 455 GAGGATTTGCTGATGCAAAAGAGCTGATTTCTTCTCTCCGACGATTTCTTCTGCA 514
Qy 393 CAAGTCTCTGCTGCTGCTGCTGCAAAACAAAGATTGATCCGATCGCTTCTTCTGAAAG 452
Db 515 AATGTTCCATTTCTCATCTTCTTGGCAACAAAGATTGATCCGATGCTGCTCTGAAAG 574
Qy 453 GAGTTGCGGTTCACATTTGGGTGACCA--TGACCACTGTGTAAAGAACGCTGACCTG 509
Db 575 GAGTGGCGGTTCACATTTGAGGCTTTCAGCAACTTTCACACCGGGAAGGCAAGTCAACCTT 634
Qy 510 GGAATAGCAACATTTGGGCGCATTTGAGGTTTTCATGTCAGATTTGTCGCAAAATGGGG 569
Db 635 GGCACCTCCAAATGTCGGGCACTTGAAGTTTTCATGTCAGATTTGTCGCAAGATGGGC 694
Qy 570 TACCGTGAAGGTTTCAAGTGATGACCCAGTACATCAAGT 609
Db 695 TACCGCATGTTTCAAGTGATGCTCCCAATACATCAAGT 734

RESULT 15
AD081658
ID AD081658 standard; cDNA; 1073 BP.
XX
AC AD081658;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 378.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX

PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TAB/) TABASKA J B.
PA (CAO/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JB, Cao Y,
XX
DR WPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 378; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 1073 BP; 242 A; 271 C; 294 G; 266 T; 0 U; 0 Other;
XX
Query Match 49.5%; Score 330.4; DB 13; Length 1073;
Best Local Similarity 74.3%; Pred. No. 3,3e-103;
Matches 431; Conservative 0; Mismatches 146; Indels 3; Gaps 1;
Qy 33 ATGTTCTTGTAGATGGTTTAAAGCGCTTCTTSCGAGCATAGGGCTGTGGCAAGAG 92
Db 177 ATGTTCTTGTAGATGGTTTAAAGCGGTGTGGCTTCTTSCGAGCATAGGGCTGTGGCAAGAG 236
Qy 93 GCCAAAATCTGTTTCTGGGTCTCGACAAATGCTGGCAAGACTCTTCTGACATGCTC 152
Db 237 GCGAAGATCTCTTCTCTGCGCTCGACAAACGCGGCAAGACACGCTGCTCCACATGCTC 296
Qy 153 AAGGATGAGAAACCTGGGCAACATCAACCAACGAGATCAAGATCAAGAGAGTTAGT 212
Db 297 AAGGACGAGCGGTGTGGCAACGACCGACGACCGACGACGTCGAGAGAGCTGAC 356
Qy 213 ATCAACAGATGAGATTCAAGCATTTGATCTGGGTGGCCACACAAATGCTCGACGGCTG 272
Db 357 ATCGGCAAGATCAAGATTCAAGGCTTTCGACTCGGCGGCAACGAGATCGGCGCGGCTC 416
Qy 273 TGGAGGACTACTATGCTAAGTGTGATGCTATGATGCTTCTGACGAGTACAGAG 332
Db 417 TGGAGGATTTACTACGCAAGGTTGATGCTGATGATACCTGATGATGATGATGATG 476
Qy 333 GAGGATTTGCTGATGCAAAAGAGAGCTGATTTCTTCTCTCCGACGATCTCTGCTCC 392
Db 477 GAGGATTTGCTGATGCAAAAGAGAGCTGATTTCTTCTCTCTGTCAGATGATTTCTTGGCA 536
Qy 393 CAAGTCTCTGCTGCTGCTGCTGCAAAACAAAGATTGATCCGATCGCTTCTTCTGAAAG 452
Db 537 AATGTTCCATTTCTCATCTTCTTGGCAACAAAGATTGATCCGATGCTGCTCTGAAAG 596
Qy 453 GAGTTGCGGTTCACATTTGGGTGACCA--TGACCACTGTGTAAAGAACGCTGAACTG 509
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Db 597 GAGCTGCGGTATGCACCTTAGCCCTTAGCACTTCACAACCGGGAAGGCAAGTCAACCTT 656
QY 510 GGAGATAGCAACATTCGGGCCCATTTGAGGTTTCATGTGACATATTGTGGCAAAATGGGG 569
Db 657 GCGGACTCCAAATGTCCGGCCACTTGAAGTTTCAATGTCAAGTGTGTTCCCAAGATGGGC 716
QY 570 TACGGTGAAGGTTTCAAGTGATGACCCAGTACATCAAGT 609
Db 717 TACGGCGATGTTCAAAGTGGTCTCCCAATACATCAAGT 756

Search completed: December 8, 2005, 23:08:48
Job time : 480 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2005, 21:24:11 ; Search time 3748 Seconds
(without alignments)
8326.303 Million cell updates/sec

Title: US-10-688-481-6

Perfect score: 667

Sequence: 1 atcccgagcgctagatcacc.....taagagcgagcgtaacgc 667

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

EST:*

1: gb_ests1:*
2: gb_ests2:*
3: gb_ests3:*
4: gb_ests4:*
5: gb_ests5:*
6: gb_ests6:*
7: gb_ests7:*
8: gb_ests8:*
9: gb_ests9:*
10: gb_ests10:*
11: gb_ests11:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	518	77.7	596	3	BJ581337
C 2	482.6	72.4	734	3	BJ598350
C 3	482.6	72.4	740	3	BJ609449
C 4	482.2	72.3	650	3	BJ599136
C 5	474.2	71.1	607	3	BJ595512
C 6	433	64.9	502	3	BJ581125
C 7	404.8	60.7	528	3	BJ607298
C 8	402.8	60.4	638	3	BJ173605
C 9	401.4	60.2	567	3	BJ171787
C 10	392.4	58.8	861	7	CN206979
C 11	371.8	55.7	600	3	BJ595842
C 12	358.8	53.8	565	3	BJ169845
C 13	345.8	51.8	684	3	BJ941869
C 14	343	51.4	751	7	CK748609
C 15	343	51.3	749	3	BJ572166
C 16	342	51.3	795	8	DR955634
C 17	342	51.3	846	2	DR798487
C 18	341.6	51.2	501	2	BG361861
C 19	340.4	51.0	738	8	DN221038
C 20	339.8	50.9	887	7	CO444180
C 21	339.8	50.9	887	7	CO444180
C 22	339.4	50.9	810	7	CO518930

C	23	339	50.8	766	8	DR798486	DR798486	ZM_BPB002
	24	337.2	50.6	695	6	CD880780	CD880780	FL.075N23
	25	337.2	50.6	823	7	CO444711	CO444711	MZCC11007
	26	337.2	50.6	907	7	CN128660	CN128660	RHOH.30
	27	337.2	50.6	933	7	CO443833	CO443833	MZCC11006
	28	336.2	50.4	646	2	BE494747	BE494747	WHE127-G
	29	335.6	50.3	708	4	CO722843	CO722843	MDdb501e
	30	335.6	50.3	1098	4	AY106333	AY106333	Zea_mays
	31	335.2	50.3	859	1	AJ822454	AJ822454	AT822454
	32	335	50.2	676	7	CN201215	CN201215	Tor1235 G
	33	334	50.1	638	5	BU037417	BU037417	946138F10
	34	334	50.1	724	5	BQ779008	BQ779008	946116C06
	35	334	50.1	1121	4	AY104010	AY104010	Zea_mays
	36	333	49.9	1152	8	DR736886	DR736886	FGAS08225
	37	332.8	49.9	669	5	BU098049	BU098049	946123E11
	38	332.4	49.8	720	7	CO526683	CO526683	3530.1.17
	39	332.4	49.8	830	7	DR829325	DR829325	ZM_BPB007
	40	332.4	49.8	877	8	DR824574	DR824574	ZM_BPB006
	41	331.8	49.7	797	6	CF446497	CF446497	EST682842
	42	331.8	49.7	872	6	CF214955	CF214955	CAS70001
	43	331.2	49.7	636	5	BU827781	BU827781	K008P84P
	44	330.6	49.6	589	6	CA825610	CA825610	R62D03 tV
	45	330.4	49.5	863	7	CN144473	CN144473	WOUNDI_22

ALIGNMENTS

RESULT 1
BJ581337/c
LOCUS
DEFINITION
BJ581337 normalised full length cDNA library, chloronemata,
caulonemata and malformed buds Physcomitrella patens subsp. patens
cDNA clone pphid16D19 3', mRNA sequence.

ACCESSION
BJ581337
VERSION
BJ581337.1 GI:37823271
KEYWORDS
EST.
SOURCE
Physcomitrella patens subsp. patens
ORGANISM
Physcomitrella patens subsp. patens
Bryophyta; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.

REFERENCE
1 (bases 1 to 596)
Nishiyama,T., Fujita,T., Shin-I,T., Seki,M., Nishide,H.,
Uchiyama,I., Kamiya,A., Carinici,P., Hayashizaki,Y., Shinozaki,K.,
Kohata,Y. and Haasbe,M. Carinici,P., Hayashizaki,Y., Shinozaki,K.,
Comparative genomics of Physcomitrella patens gametophytic
transcriptome and Arabidopsis thaliana: implication for land plant
evolution

TITLE

JOURNAL
PUBMED
COMMENT
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
12808149
Contact: Tadao Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855

Email: tshin@genetics.nig.ac.jp
A backbone of the vector is basically from pBluescript II (KS),
that was in vivo excised from a 1-PLC phage vector (Carinici et al.,
2001). 5' end of the cDNA that was digested with XhoI was ligated
to SalI site of the vector and the 3' end including polyA tail was
ligated to BamHI site of the
vector(5'- gagAgaAgagatCCACCTGAGAGTTTGTGTTTGTGTTT-3' was
used as a 1st 3' primer, and
5'-gggtTCGAGTCATCTGTCAGACGAGTGAAGTGAAGCCGNNNN-3' as 2nd
primer, giving the following 5' leader sequence,
AGGCAATCGCGAGCTCGATTCGAGACCG). cDNA insert could be
amplified with conventional T7 and T3 primers. This full-length
cDNA library was generated according to the method described in
Nishiyama et al. (2003).
Protonemata were blended by the POLYTRON, and then cultivated on
the BCDATG medium for 13-14 days under the continuous light.
These clones are available from RIKEN Bio Resource Center

(http://www.brc.riken.go.jp/lab/epd/Eng/index.html). The database of Physcomitrella EST clones is available at the PHYSCODbase (http://mosa.nibb.ac.jp).

FEATURES

Location/Qualifiers

1..596
/organism="Physcomitrella patens subsp. patens"
/mol_type="mRNA"
/sub_species="patens"
/db_xref="taxon:145481"
/clone="pphb16b19"
/issue_type="mixture of chloronemata, caulonemata and malformed buds"
/clone_lib="normalized full length cDNA library,
chloronemata, caulonemata and malformed buds"

ORIGIN

Query Match 77.7%; Score 518; DB 3; Length 596;
Best Local Similarity 100.0%; Pred. NO. 7.7e-145; Indels 0; Gaps 0;
Matches 518; Conservative 0; Mismatches 0;

142 TGACATGCTCCAGATGAGAACTGGGGCAACATCAACCAACGAGTATCCAACTCAG 201
143 TGGACATGCTCCAGATGAGAACTGGGGCAACATCAACCAACGAGTATCCAACTCAG 201
596 TGGACATGCTCCAGATGAGAACTGGGGCAACATCAACCAACGAGTATCCAACTCAG 537
202 AGGAGTTGAGTATCAACAGAGTGAAGTTCAAGATTCGATCTGGTGGCCACATCG 261
536 AGGAGTTGAGTATCAACAGAGTGAAGTTCAAGATTCGATCTGGTGGCCACATCG 477
262 CTGACGCGGTGGAGGGAGTACTATGCTAAGTGAAGTATGATGATCTGGTGGCCAC 321
476 CTGACGCGGTGGAGGGAGTACTATGCTAAGTGAAGTATGATGATCTGGTGGCCAC 417
322 CAGTAGACAGGAGAGATTTGCTGATCAAGAAAGAGCTGATCTCTCTCCGACG 381
416 CAGTAGACAGGAGAGATTTGCTGATCAAGAAAGAGCTGATCTCTCTCCGACG 357
382 ATTCTGCTCCCAAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 441
356 ATTCTGCTCCCAAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 297
442 CTTCGTAAGAGAGATGGCGGTTCACTGGGTTGACACATGACACATGGTAAAGAACG 501
296 CTTCGTAAGAGAGATGGCGGTTCACTGGGTTGACACATGACACATGGTAAAGAACG 237
502 TGAACCTGGAGATAGCAACATTCGCCCATTTGAGTTTCAATGAGTATTTGGCGCA 561
236 TGAACCTGGAGATAGCAACATTCGCCCATTTGAGTTTCAATGAGTATTTGGCGCA 177
562 AAATGGGATACGGTGAAGGTTTCAAGTGAATGACCCAGTACATCAAGTATTTGCT 621
176 AAATGGGATACGGTGAAGGTTTCAAGTGAATGACCCAGTACATCAAGTATTTGCT 117
622 GTGAAAGAGAACTTAGCTGGGTGTTTAAGACGCGCA 659
116 GTGAAAGAGAACTTAGCTGGGTGTTTAAGACGCGCA 79

RESULT 2
BJS98350/c 734 bp mRNA linear EST 22-OCT-2003
DEFINITION BJS98350 normalized full length cDNA library, chloronemata,
caulonemata and rhizoid-like protonemata Physcomitrella patens
subsp. patens cDNA clone pphn23e05 3', mRNA sequence.

ACCESSION BJS98350.1 GI:37840342

KEYWORDS

Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens

SOURCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryophyta; Funariidae; Funariaceae; Funariaceae; Physcomitrella.

REFERENCE

1 (bases 1 to 734)
Nishiyama, T., Fujita, T., Shin-i, T., Seki, M., Nishide, H.,
Uchiyama, I., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K.,

TITLE

Kohara, Y. and Hasebe, M.
Comparative genomics of Physcomitrella patens gametophytic
transcriptome and Arabidopsis thaliana: implication for land plant
evolution

Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)

JOURNAL

12808149

PUBLISHED

12808149

COMMENT

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Email: tshin@genes.nig.ac.jp
A backbone of the vector is basically from pBluescript II (KS),
that was in vivo excised from a 1-FLC phase vector (Carninci et al.
2001). 5' end of the cDNA that was digested with XhoI was ligated
to SalI site of the vector and the 3' end including polyA tail was
ligated to BamHI site of the
vector (5'-gagagagagagatccaaacctggagaggtttttttttttttttttt-3' was
used as a 1st 3' primer, and
5'-gggtctcgagtcgctgttccagacagcgatgactcgagaaacggnnnn-3' as 2nd
5'-hairpin primer, giving the following 5' boarder sequence,
AGGCCAAATCCGCGAGCTCGATTCGATTCGAGAACCG). cDNA insert could be
amplified with conventional T7 and T3 primers. This full-length
cDNA library was generated according to the method described in
Nishiyama et al. (2003).
Protonemata were blended by the POLYTRON, and then cultivated on
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of Physcomitrella EST clones is available at the PHYSCODbase
(http://mosa.nibb.ac.jp).

FEATURES

source

Location/Qualifiers
1..734
/organism="Physcomitrella patens subsp. patens"
/mol_type="mRNA"
/sub_species="patens"
/db_xref="taxon:145481"
/clone="pphb16b19"
/issue_type="mixture of chloronemata, caulonemata and
rhizoid-like protonemata"
/clone_lib="normalized full length cDNA library,
chloronemata, caulonemata and rhizoid-like protonemata"

ORIGIN

Query Match 72.4%; Score 482.6; DB 3; Length 734;
Best Local Similarity 85.2%; Pred. No. 4e-134;
Matches 539; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

5 CGGGTCGTAAGATACCAAGGCTGGTACCATGTTCTTGTGATGTTGTTTACGGCTTCT 64
635 CGAGCCGCGCAGATGTTAAGCTCGCATCATGTTATCGTGAATGGTTTATGCTTCT 576
65 TGGAGATGATGGGCTGTGGAGAGAGGCAAAATCTGTTCTGGGCTCGACATGC 124
575 TGGAGATGATGGTGTGGAGAGAGGCAAAATCTGTTCTGGGCTCGACATGC 516
125 TGGCAAGACTACTCTTCTGCACATGCTCAAGATGAGAACTGGGGCAACATCAACCAAC 184
515 CGGGAAGACGACCTTCTGCACATGCTCAAGATGAGAACTGGGGCAACATCAACCAAC 456
185 GCAGTATCCAAAGCTCAGAGAGGTTGATGATCAACAGATGAAGTTCAAGCATTCGATCT 244
455 GCAGTATCCAAAGCTCAGAGAGGTTGATGATCAACAGATGAAGTTCAAGCATTCGATCT 396
245 GGGTGGCCACACATGCTCGACGCGTGTGAGAGGACTATATGCTTAAGTGGATGCTAT 304
395 AGGTGGTCAACACATGCTCGACGCGTGTGAGAGGACTATATGCTTAAGTGGATGCTAT 336
305 AGGTATCTGCTGAGACGACATGACAGAGGAGATTTGCTGAGTCAAGAAAGAGCTCGA 364
335 GCTTACCTTGTGACGACGACATTTGACAGAGAGGTTTCTGTAATCAAGAAAGAGCTCGA 276

QY 365 TTCTCTCTCTCCGACGATTTCTGTCCCAAGTTCTGTGCTGCTCGGAAACAAGAT 424
| | | | |
Db 275 CTCCTTGCTCTCGGAGTACCTCGCTCCCAAGGCGCTGTGCTGCTTGGCAACAAGAT 216
| | | | |
QY 425 TGAATATCCGATGCGCTTTCTTGAAGACGAGTTGCGGTTCACTTTGGTTGACCAATGAC 484
| | | | |
Db 215 TGACATCCCTTACGCTGCTCCCAAGATGATATGCGGTACACACTGCGGCTGACATGAC 156
| | | | |
QY 485 CACTGTAAAGGAAGGATGAACTGGGAGATAGCAATTCGCGCCATTGAGGTTTCAT 544
| | | | |
Db 155 CACTGCAAGGAAGGAGGATGAACTGAAAGATAGCAATTCGCGCCATTGAGGTTTCAT 96
| | | | |
QY 545 GTGCACTATTTGTCGCAAAATGGGATGAGGTTTCAAGTGAATGACCAATGATACAT 604
| | | | |
Db 95 GTGCACTATTTAGTCCGTAAGATGGGTTTACGCGCAAGGTTCAATGATGATGACGAGTATAT 36
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QY 605 CAAATGATTTGTTTCTGTGAAAGAGAACTTA 637
| | | | |
Db 35 TAAATGATTTGTTTGAATAGACAAGAAAGTAA 3
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RESULT 3
Bu609449/c 740 bp mRNA linear EST 22-OCT-2003
LOCUS Bu609449 normalized full length cDNA library, chloronemata,
DEFINITION caulonemata and rhizoid-like protonemata Physcomitrella patens
subep. patens cDNA clone pphn47g10 3', mRNA sequence.
Bu609449
Bu609449.1 GI:37851441
EST.
Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
1 (bases 1 to 740)
Nishiyama,T., Fujita,T., Shin-I,T., Seki,M., Nishide,H.,
Uchiyama,I., Kamiya,A., Carinici,P., Hayashizaki,Y., Shinozaki,K.,
Kohara,Y. and Hasebe,M.
Comparative genomics of Physcomitrella patens gametophytic
transcriptome and Arabidopsis thaliana: implication for land plant
evolution
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
12808149
Contact: Tadasu Shin-I
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A backbone of the vector is basically from pBluescript II (KS),
that was in vivo excised from a 1-F1C phage vector (Carinici et al.
2001). 5' end of the cDNA that was digested with XhoI was ligated
to SalI site of the vector and the 3' end including polyA tail was
ligated to BamHI site of the
vector(5'- GAGAGAGAGAGATCCACCTGGAGAGTCTTTTCTTTTCTTTVN-3' was
used as a 1st 3' primer, and
5'-gggttcgagtcgacgtgttcgacacagcagatgactcgagacccgannnn-3' as 2nd
5'-hairpin primer, giving the following 5' boarder sequence,
AGCCCAATCGGCGCGGATTCGTAATTCGTCGACACCG. cDNA insert could be
amplified with conventional T7 and T3 primers. This full-length
cDNA library was generated according to the method described in
Nishiyama et al. (2003).
Protonemata were blended by the POLYTRON, and then cultivated on
the BCDAG medium for 13- 14 days under the continuous light.
These clones are available from RIKEN Bio Resource Center
(http://www.brc.riken.go.jp/lab/epd/Eng/index.html). The database
of Physcomitrella EST clones is available at the PHYSCDBase
(http://mosb.nibb.ac.jp).
Location/Qualifiers
1..740
/organism="Physcomitrella patens subsp. patens"
/mol_type="mRNA"

/sub_species="patens"
/db_xref="taxon:145481"
/clone="pphn47g10"
/tissue_type="mixture of chloronemata, caulonemata and
rhizoid-like protonemata"
/clone_lib="normalized full length cDNA library,
chloronemata, caulonemata and rhizoid-like protonemata"

ORIGIN

Query Match 72.4%; Score 482.6; DB 3; Length 740;
Best Local Similarity 85.2%; Pred. No.4e-114;
Matches 539; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 5 CGGTCCTGATGATACCAAGGCTGTGATCAATGTTCTTTGATATGGTTTACGGCTTTCT 64
| | | | |
Db 633 CGAGCCGAGATGTTTAACCTCGATCATGTTTATCGTAAATGGTTTATGCGCTTCT 574
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QY 65 TCGAGCATAGGCGCTGTGCGAAGAGGCGCAAAATCTGTTTCTGTGGTCTGACATATC 124
| | | | |
Db 573 TCGAGCATATGAGTTGTGTGAGAGAGGCGCAAAATCTGTTTCTGTGGTCTGACATATC 514
| | | | |
QY 125 TGGCAAGATCTCTTCTGCAATGCTCAAGATGAGAACTGGGCGAATCAACCAAC 184
| | | | |
Db 513 CGGGAAGAGACATCTTGTGACATGCTCAAGATGAGAACTGGGCGAATCAACCAAC 454
| | | | |
QY 185 GCAGTATCCACGTCGAGAGAGTGTGATCAACAGAGTGAAGTTCAAGCATTCGATCT 244
| | | | |
Db 453 GCAGTATCCACATCTGAAAGATTTAGCATCATAGGTTGAAGTTCAAGCATTCGATCT 394
| | | | |
QY 245 GGGTGGCCACACATGCTGACGCGGTGTGAGAGGACTATGCTTAAGTGGATCTAT 304
| | | | |
Db 393 AGGTGGTCAACGATTTGCTGACGTGTGTGAGGAGCTACTATGCTTAAGTGGATCTAT 334
| | | | |
QY 305 AGGTATCTCTGTCGACGAGTATGACGAGGAGATTTGCTGATCAAGAAAGAGTCCA 364
| | | | |
Db 333 CGTTTACCTTGTGCAAGGAGTGAAGAGAGTTCTTGATCAAGAAAGAGTCCA 274
| | | | |
QY 365 TTCTCTCTCTCCGACGATTTCTGTGCCAAGTTCTGTGCTGCTCGGAAACAAGAT 424
| | | | |
Db 273 CTCCTTGCTCTCGGAGTACCTCGCTCCCAAGGCGCTGTGCTGCTTGGCAACAAGAT 214
| | | | |
QY 425 TGAATATCCGATGCGCTTTCTTGAAGACGAGTTGCGGTTCACTTTGGTTGACCAATGAC 484
| | | | |
Db 213 TGACATCCCTTACGCTGCTCCGAAGATGATATGCGGTACACACTGCGCTGACATGAC 154
| | | | |
QY 485 CACTGTAAAGGAAGGATGAACTGGGAGATGACCAATTCGCGCCATTGAGGTTTCAT 544
| | | | |
Db 153 CACTGCAAGGAAGGAGGATGAACTGGAAGATGACCAATTCGCGCCATTGAGGTTTCAT 94
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QY 545 GTGCACTATTTGTCGCAAAATGGGATGAGGTTTCAAGTGAATGACCAATGATACAT 604
| | | | |
Db 93 GTGCACTATTTAGTCCGTAAGATGGGTTTACGCGCAAGGTTCAATGATGATGACGAGTATAT 34
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QY 605 CAAATGATTTGTTTCTGTGAAAGAGAACTTA 637
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Db 35 TAAATGATTTGTTTGAATAGACAAGAAAGTAA 1
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RESULT 4
Bu599136 650 bp mRNA linear EST 22-OCT-2003
LOCUS Bu599136 normalized full length cDNA library, chloronemata,
DEFINITION caulonemata and rhizoid-like protonemata Physcomitrella patens
subep. patens cDNA clone pphn25113 3', mRNA sequence.
Bu599136
Bu599136.1 GI:37841128
EST.
Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
1 (bases 1 to 650)
Nishiyama,T., Fujita,T., Shin-I,T., Seki,M., Nishide,H.,

TITLE

Uchiyama, I., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K., Kohara, Y. and Hasebe, M.
Comparative genomics of *Physcomitrella patens* gametophytic transcriptome and *Arabidopsis thaliana*: implication for land plant evolution

JOURNAL: Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
PUBMED: 12808149
COMMENT: Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp

A backbone of the vector is basically from pBluescript II (KS), that was in vivo excised from a 1-PLC phage vector (Carninci et al., 2001). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector (5'-GAGAGAGAGAGATCCCAACCTGgAgATTTTTTTTTTTTNN-3' was used as a 1st 3' primer, and 5'-ggttcctgagtcgctgctgtccagacagcgatgactcgagAACGNNNNN-3' as 2nd 5'-hairpin primer, giving the following 5' boarder sequence. AGCCCAATCGCCGACCTGCAATTGTCGAGAACG). cDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated according to the method described in Nishiyama et al. (2003).
Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (<http://www.brc.riken.go.jp/lab/epd/Eng/index.html>). The database of *Physcomitrella* EST clones is available at the PHYSCoBase (<http://mos.nibb.ac.jp/>).

FEATURES
source
location/Qualifiers

1..650
/organism="Physcomitrella patens subsp. patens"
/mol_type="mRNA"
/db_xref="taxon:145481"
/clone="pPhn25113"
/tissue_type="mixture of chloronemata, caulonemata and rhizoid-like protonemata"
/clone_lib="normalized full length cDNA library,
chloronemata, caulonemata and rhizoid-like protonemata"

ORIGIN

Query Match 72.3%; Score 482.2; DB 3; Length 650;
Best Local Similarity 85.3%; Pred. NO. 5.1e-134;
Matches 538; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 5 CGGGTCCGTAGATACCAAGCTGTGATCCATGTTCTGTGTAGATTGGTTTACGGCTTCT 64
DB CGAGCCGCGACATGTAAAGCTGCGATCATGTTTATCTGATGATTTGTTTATGCTTTCT 572
QY 65 TGCAGCATAGAGGCTGTGGCAAGAGAGGCCAAATCTGTTTGTGGTCTGCAAAATGC 124
DB TGCAGCATAGAGGCTGTGGCAAGAGAGGCCAAATCTGTTTGTGGTCTGCAAAATGC 512
QY 125 TGGCAAGCTACTCTTCTGCAACATGCTCAAGATGAGAACTGGGGCAACATCAACAAC 184
DB CGGGAAGCGACACTTCTGCAACATGCTCAAGATGAGAACTGGGGCAACATCAACAAC 452
QY 185 GCAGATATCAACGTCAGAGAGATTGATGATCAACAGATGAAGTTCAAGCATTCGATCT 244
DB GCAATATCAACATCTGAAAGATTGAGATCAATAGGTGAAGTTCAAGCATTCGATCT 392
QY 245 GAGTGGCCACCAATTCGTCGACGCGTGTGAGAGGACTACTATGCTAAAGTGATCTAT 304
DB AAGTGTGACACAGATGCTGACGCGTGTGAGAGGACTACTATGCTAAAGTGATCTAT 332
QY 305 AGTGTATCTGTCGACGAGTGAACAGGAGAGATTTGCTAGTCAAGAAAGAGCTTGA 364
DB CGTTTACTTGTGACGAGTGAACAGGAGAGATTTGCTAGTCAAGAAAGAGCTTGA 272

QY 365 TTCTCTTCTCTCCGACGATTTCTGTGCCAGTCTCTGTGCTGTCTCGGAAACAAGAT 424
DB CTCTCTGCTCTCGAGATGATCGCTCTCCCAAGGCTGTGCTGTCTCTGGCAACAAGAT 212
QY 425 TGAATCCGCTAGCTTCTCTGAAAGAGGTTGGGGTTCACACTTGGGTTGACATGAC 484
DB TGAATCCGCTAGCTTCTCTGAAAGATGATTTGCGTACACCTGGCTTGACATGAC 152
QY 485 CACTGTAAAGAACCGGTGAACCTGGAGATGACCAATTGCGCCCATTTAGGTTTCAT 544
DB CACTGTAAAGAACCGGTGAACCTGGAAGATGACCAATTGCGCCCATTTAGGTTTCAT 92
QY 545 GTCCAGTATTGTCGCAAAATGGGGTACCGTGAAGTTTCAAGTGATGACCAATGAT 604
DB GTCCAGTATTGTCGCAAAATGGGGTACCGGCGAAGGTTCAAGTGATGACCAATGAT 32
QY 605 CAAGTATTGTTTCTCTGTGAAGAGAACT 635
DB TAAATATTGTTTGAATGACAAAGAAAGT 1

RESULT 5
LOCUS BJ952512/c 607 bp mRNA linear EST 14-JUN-2005
DEFINITION patens cDNA clone pPhn16p22 3', mRNA sequence.
ACCESSION BJ952512
VERSION BJ952512.1 GI:67692279
KEYWORDS EST.
SOURCE Physcomitrella patens subsp. patens
ORGANISM Physcomitrella patens subsp. patens
Bryophyta; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.

REFERENCE
AUTHORS Fujita, T., Nishiyama, T., Shin-i, T., Kohara, Y. and Hasebe, M.
TITLE Physcomitrella patens EST at a stage of the first asymmetric cell division of protonema
JOURNAL Unpublished (2005)
COMMENT Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp

Protonemata were inoculated on BCDATG medium for every ca. 5 days. Protoplasts were isolated from the protonemata, further incubated at 25C under continuous light for 2-3 days. The regenerated cells, which were rich in cells at a stage during the first asymmetric cell division, were collected. Total RNA was extracted for constructing a full-length cDNA library. The database of the EST clones is available at the PHYSCoBase (<http://mos.nibb.ac.jp/>).

FEATURES

source

1..607
/organism="Physcomitrella patens subsp. patens"
/mol_type="mRNA"
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/dev_stage="at the first asymmetric cell division of protoplasts"
/clone_lib="pPhn full-length cDNA library"
/note="Protonemata were inoculated on BCDATG medium for every ca. 5 days. Protoplasts were isolated from the protonemata, further incubated at 25C under continuous light for 2-3 days. The regenerated cells, which were rich in cells at a stage during the first asymmetric cell division, were collected. Total RNA was extracted for constructing a full-length cDNA library."

ORIGIN

Query Match 71.1%; Score 474.2; DB 3; Length 607;
 Best Local Similarity 86.3%; Pred. No. 1.3e-111;
 Matches 524; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 6 GGGTCGTAATACCAAGGCTGCTACCATGTTCTGTAGATGTTTACGGCTTTCTT 65
 DB 607 GACCCCGAGATGTTAAGCTGCGATCATCTTTATCTAGATGTTTATGCTTTCTT 548
 QY 66 GCGAGCATAGGGCTGCGAGAGAGGCGAAATCCGTTTCGGGCTCGCAATGCT 125
 DB 547 GCGAGCATAGGGCTTGGCGAGAGAGGCGAAATCTGTTCTGGGCTTGGCAATGCC 488
 QY 126 GCGAAGCTACTCTTCTGCACTGCTCAAGATGAGAACTGGGGCAATCAACCAACG 185
 DB 487 GCGAAGCTACTCTTCTGCACTGCTCAAGATGAGAACTGGGGCAATCAACCAACG 428
 QY 186 CAGTATTCACAGTCAGAGAGTTGAGTATCAACAGATGAAGTTCAAGCATTCGATCTG 245
 DB 427 CAGTATTCACAGTCAGAGAGTTGAGTATCAACAGATGAAGTTCAAGCATTCGATCTA 368
 QY 246 GGTGGCCACACATCGCTCGACGGGTGAGGGGACTACTATGCTAAGTGAAGTCTATA 305
 DB 367 GGTGGTCACAGATGCTCGACGGGTGAGGGGACTACTATGCTAAGTGAAGTCTATC 308
 QY 306 GTGATCTCGTCGACGAGTGAACAGGAGAGATTTGCTGAGTCAAGAAAGAGCTCGAT 365
 DB 307 GTTACTCTTCTGACGAGTGAACAGGAGAGATTTGCTGAGTCAAGAAAGAGCTCGAC 248
 QY 366 TCTCTTCTCTCGACGATGCTGTCGCAAGTTCTGCTGCTGCTGCGGAAACAAGATT 425
 DB 247 TCTCTGCTCTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 188
 QY 426 GATATCCCGTACGCTTTCTTGAAGAGAGTGGGCTTCACTTGGGTTGACCATACACC 485
 DB 187 GATATCCCGTACGCTTTCTTGAAGAGAGTGGGCTTCACTTGGGCTTCACTTGGGCTTCACT 128
 QY 486 ACTGTTAAAGAAAGCGGTAAGCTGGAGATAGCAACATTCGGCCATTGAGTTTCATG 545
 DB 127 ACTGTTAAAGAAAGCGGTAAGCTGGAGATAGCAACATTCGGCCATTGAGTTTCATG 68
 QY 546 TGCAGTATTTGCGCAAAATGGGGTACGGTGAAGTTTCAAGTGAATGACCCAGTATATC 605
 DB 67 TGCAGTATTTGCGCAAAATGGGGTACGGGTTACGCGAAGGTTTCAAGTGAATGACCCAGTATAT 8
 QY 606 AAGTGAT 612
 DB 7 AAGTGAT 1

RESULT 6
 BUS81125/c 502 bp mRNA linear EST 22-OCT-2003
 LOCUS BUS81125 normalized full length cDNA library, chloronemata,
 DEFINITION caulonemata and malformed buds Physcomitrella patens subsp. patens
 accession BUS81125
 cDNA clone phb16K02 3', mRNA sequence.
 VERSION BUS81125.1 GI:37823059
 SOURCE EST.
 ORGANISM Physcomitrella patens subsp. patens
 Physcomitrella patens subsp. patens
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
 1 (bases 1 to 502)
 Nishiyama, T., Fujita, T., Shin-i, T., Seki, M., Nishide, H.,
 Uchiyama, I., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K.,
 Kohara, Y. and Hasebe, M.
 Comparative genomics of Physcomitrella patens gametophytic
 transcriptome and Arabidopsis thaliana: implication for land plant
 evolution
 Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
 JOURNAL PUBMED
 COMMENT 12808149
 Contact: Tadasu Shin-i
 Center For Genetic Resource Information

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 1111 Yatae, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp
 A backbone of the vector is basically from pBluescript II (KS),
 that was in vivo excised from a 1-FLC phage vector (Carninci et al.
 2001). 5' end of the cDNA that was digested with XhoI was ligated
 to SalI site of the vector and the 3' end including polyA tail was
 ligated to BamHI site of the
 vector(5'-gagagagagagatccacacctggagaggtttttttttttttttt-3' was
 used as a 1st 3' primer, and
 5'-ggttctgagtcagtcgtctgtccagacgagatgactgagaaacccgannnn-3' as 2nd
 5'-hairpin primer, giving the following 5' boarder sequence,
 AGGCCAAATCGCGAGTCCGATTCGAGAACCG). cDNA insert could be
 amplified with conventional T7 and T3 primers. This full-length
 cDNA library was generated according to the method described in
 Nishiyama et al. (2003).
 Protonemata were blended by the POLYTRON, and then cultivated on
 the BCDATG medium for 13-14 days under the continuous light.
 These clones are available from RIKEN Bio Resource Center
 (http://www.brc.riken.go.jp/lab/epd/Eng/index.html). The database
 of Physcomitrella EST clones is available at the PHYSCODbase
 (http://moss.nibb.ac.jp).
 Location/Qualifiers
 1..502
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 /db_xref="taxon:1145481"
 /clone="ppb16K02"
 /issue_type="mixture of chloronemata, caulonemata and
 malformed buds"
 /clone_lib="normalized full length cDNA library,
 chloronemata, caulonemata and malformed buds"

ORIGIN

Query Match 64.9%; Score 433; DB 3; Length 502;
 Best Local Similarity 99.3%; Pred. No. 3.5e-119;
 Matches 433; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 224 GAAGTTCAAGACATTCGATCTGGGTGGCCACACATCGCTCGACGGGTGAGGAGCTA 283
 DB 502 GAAGTTCAAGACATTCGATCTGGGTGGCCACACATCGCTCGACGGGTGAGGAGCTA 443
 QY 284 CTATGCTTAAGTGTGATCTATGATCTCTGTCGACGCACTGACAGGAGAGATTGC 343
 DB 442 CTATGCTTAAGTGTGATCTATGATCTCTGTCGACGCACTGACAGGAGAGATTGC 383
 QY 344 TGAATCAAGAAAGACCTGATCTCTCTCTCGACGATTCCTGCTCCCAATTCCTGT 403
 DB 382 TGAATCAAGAAAGACCTGATCTCTCTCTCTCGACGATTCCTGCTCCCAATTCCTGT 323
 QY 404 GCTCGTCTGGGAAACAAGTTGATATCCCGTACGGCTTCTTCTGAAGACGAGTTGGCTT 463
 DB 322 GCTCGTCTGGGAAACAAGTTGATATCCCGTACGGCTTCTTCTGAAGACGAGTTGGCTT 263
 QY 464 CACACTTGGGTTGACATGACCACTGTTAAAGAAACGCTGGAACCTGGAGATTCGAAT 523
 DB 262 CACACTTGGGTTGACATGACCACTGTTAAAGAAACGCTGGAACCTGGAGATTCGAAT 203
 QY 524 TCGGCCCATTTAGAGTTTCAATGTCAGATTTGAGCCAAATAGGGGATCGGTAAGGTTT 583
 DB 202 TCGGCCCATTTAGAGTTTCAATGTCAGATTTGAGCCAAATAGGGGATCGGTAAGGTTT 143
 QY 584 CAAGTGATGACCCAGTATCAAGTATGTTTCTGTTGAAGAGAACTTAGCTCGG 643
 DB 142 CAAGTGATGACCCAGTATCAAGTATGTTTCTGTTGAAGAGAACTTAGCTCGG 83
 QY 644 TGTTTAAGCGACGA 659
 DB 82 TGTTTAAGCGACGA 67

RESULT 7
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 LOCUS
 DEFINITION 528 bp mRNA linear EST 22-OCT-2003
 BJ607298 normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata Physcomitrella patens subsp. patens cDNA clone pphn39106 3', mRNA sequence.
 BJ607298
 BJ607298.1 GI:37849290
 EST.
 Physcomitrella patens subsp. patens
 Physcomitrella patens subsp. patens
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella. 1 (bases 1 to 528)
 Uchiyama, T., Fujita, T., Shin-i, T., Seki, M., Nishide, H., Nishiyama, I., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K., Kohara, Y. and Hasebe, M.
 Comparative genomes of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: implication for land plant evolution
 Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
 12808149
 Contact: Tadao Shin-i
 Center for Genetic Resource Information
 National Institute of Genetics
 111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp
 A backbone of the vector is basically from pBluescript II (KS), that was in vivo excised from a 1-FLC phase vector (Carninci et al. 2001). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector (5'-GAGAGAGAGAGATCCAACTGGAGAGATTTTATTTTATTTVN-3' was used as a 1st 3' primer, and 5'-GGTTCGAGTATCGTCTGTCCAGACGATGATCTGAGAACGNNNN-3' as 2nd 5'-hairpin primer, giving the following 5' boarder sequence, AGGCCAAATCGCGCGAGTCAATTCGTGAGAACG). cDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated according to the method described in Nishiyama et al. (2003).
 Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (http://www.brc.riken.go.jp/lab/epd/Eng/index.html). The database of Physcomitrella EST clones is available at the PHISCODbase (http://mos.nibb.ac.jp).
 Location/Qualifiers
 1..528
 /organism="Physcomitrella patens subsp. patens"
 /mol_type="mRNA"
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 /db_xref="taxon:145481"
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 /issue_type="mixture of chloronemata, caulonemata and rhizoid-like protonemata"
 /clone_lib="normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata"

ORIGIN
 Query Match 60.7%; Score 404.8; DB 3; Length 528;
 Best Local Similarity 85.4%; Pred. No. 1.2e-110;
 Matches 451; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 110 GGGTCTGCAGATCTGGCAAGACTACTCTTCTGCACATGCTCAAGATGAGAACTGGG 169
 DB 528 GGGCTTGCAGATGCGCGAGAGACGACCTTCTGCACATGCTCAAGATGAGAACTGGG 469
 QY 170 GCAACATCAACCAACGAGTATCCAGCTCAGAGAGTTGATGATCAACAGATGAAATT 229
 DB 468 GCAACATCAACCAACGAGTATCCAGATCTGAAGAAATTGAGCATCAATAGGGTGAAGTT 409

QY 230 CAAGCATTCGATCTGGTGGCCACAAATCGCTGACCGGTGTGAGAGGACTACTATGCG 289
 DB 408 CAAGCATTCGATCTGAGTGTGTGACACGATGCTGACGTGTGTGAGAGGACTACTATGCG 349
 QY 290 TAAGGTGATGCTATAGTATCTGCTGACAGCAGATGACAGGAGAAATTTGCTAGTGC 349
 DB 348 TAAGGTGATGCTATAGTATCTGCTGACAGCAGATGACAGGAGAAATTTGCTAGTGC 289
 QY 350 AAAGAAAGACTGATCTCTCTCTCCAGATTCCTGCTCCCAAGTTCTGCTGCTGCT 409
 DB 288 AAAGAAAGACTGATCTCTCTCTCCAGATTCCTGCTCCCAAGTTCTGCTGCTGCTGCT 229
 QY 410 CTGGGAAAACAAGATTGATATCCGTAACGCTTCTTGTGAAGCAGATTGCGTTCAACT 469
 DB 228 CTTGGCAACAAGATTGATATCCGTAACGCTTCTTGTGAAGCAGATTGCGTTCAACT 169
 QY 470 TGGGTGACCATGACCACTGTGTAAGAAACGGTGAACCTGGAGATAGCAACTTGGGC 529
 DB 168 CGGCTGACCATGACCACTGTGTAAGAAACGGTGAACCTGGAGATAGCAACTTGGGC 109
 QY 530 CATTGAGTTTTCATGTGACGATATTTGTGCGCAAAATGGGGTACGGTGAAGTTTCAAGTG 589
 DB 108 CATTGAGTTTTCATGTGACGATATTTGTGCGTAAAGATGGGTACGGGAAAGTTCAAGTG 49
 QY 590 GATGACCCAGTACATCAAGTATTTTCTGTGAAAGAGAACTTA 637
 DB 48 GATGACCCAGTATATTAATGATTTTGTGCAATAGCAAGAAAGATTA 1

RESULT 8
 BJ173605/c
 LOCUS
 DEFINITION 638 bp mRNA linear EST 16-OCT-2003
 BJ173605 full length cDNA library, chloronemata and young gametophores Physcomitrella patens subsp. patens cDNA clone pphn233, mRNA sequence.
 BJ173605
 BJ173605.1 GI:18341570
 EST.
 Physcomitrella patens subsp. patens
 Physcomitrella patens subsp. patens
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella. 1 (bases 1 to 638)
 Uchiyama, T., Fujita, T., Shin-i, T., Seki, M., Nishide, H., Nishiyama, I., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K., Kohara, Y. and Hasebe, M.
 Comparative genomes of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: implication for land plant evolution
 Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
 12808149
 Contact: Tadao Shin-i
 Center for Genetic Resource Information
 National Institute of Genetics
 111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp
 A backbone of the vector is basically from pBluescript II (KS), that was in vivo excised from a 1-FLC phase vector (Carninci et al. 2001). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector (5'-GAGAGAGAGAGATCCAACTGGAGAGATTTTATTTTATTTVN-3' was used as a 1st 3' primer, and 5'-GGTTCGAGTATCGTCTGTCCAGACGATGATCTGAGAACGNNNN-3' as 2nd 5'-hairpin primer, giving the following 5' boarder sequence, AGGCCAAATCGCGCGAGTCAATTCGTGAGAACG). cDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated according to the method described in Nishiyama et al. (2003).
 Protonemata were blended by the POLYTRON, and then cultivated on

the BCDATG medium for 13-14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (<http://www.brc.riken.go.jp/lab/epd/Eng/index.html>). The database of Physcomitrella EST clones is available at the PHYSCODbase (<http://moss.nibb.ac.jp>).

FEATURES

source

Location/Qualifiers
1..638

/organism="Physcomitrella patens subsp. patens"

/mol_type="mRNA"

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/clone="pph3b23"

/issue_type="mixture of chloronemata and young gametophores with 2 to 5 leaves"

/clone_1lb="full length cDNA library, chloronemata and young gametophores"

ORIGIN

Query Match 60.4%; Score 402.8; DB 3; Length 638;
Best Local Similarity 85.4%; Pred. No. 4.8e-110; Mismatches 77; Indels 0; Gaps 0;

Matches 449; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

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112 GTCTGCACATGCTGCGCAAGACTCTTCTGACATGCTCAAGATGAGAACTGGGCG 171
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638 GTCTTGCACATGCGCGGAGACACACTTCTGACATGCTCAAGATGAGAACTGGGCG 579
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172 AACATCAACCAACGCGAGTATCCAGCTCAGAGAGTTGATCAACAGATGAAGTTCA 231
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578 AACATCAACCAACGCGAGTATCCAGCTCAGAGAGTTGATCAACAGATGAAGTTCA 519
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232 AAGCATTCGATCTGGGCGCACAACAATGCTGACGCGGTGAGAGGACTATATGCTA 291
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518 AAGCATTCGATCTGGGCGCACAACAATGCTGACGCGGTGAGAGGACTATATGCTA 459
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352 AGAAGAGCTCGATCTCTTCTCTCGACGATTTCTCTCCAAAGTTCTCTGCTGCTCC 411
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398 AGAAGAGCTCGATCTCTTCTCTCGACGATTTCTCTCCAAAGTTCTCTGCTGCTCC 339
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278 GCTGACCATGACCATGCTGTAAGAACGCTGAGATAGCAATTCGCGCCA 219
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532 TTGAGGTTTTCATGTCAGATATTTGCGCAAAATGGGGTACGGTGAAGTTTCAAGTGA 591
|||||
218 TTGAGGTTTTCATGTCAGATATTTGCGCAAAATGGGGTACGGTGAAGTTTCAAGTGA 159
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592 TGACCCAGTACATCAAGTATTTTCTCTGTAAGAGAACTTA 637
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158 TGACCCAGTACATCAAGTATTTTCTCTGTAAGAGAACTTA 113

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RESULT 9
LOCUS BUI171787 567 bp mRNA linear EST 16-OCT-2003
DEFINITION BUI171787 full length cDNA library, chloronemata and young gametophores Physcomitrella patens subsp. patens cDNA clone pph30c04 3', mRNA sequence.
VERSION BUI171787 GI:18339760
KEYWORDS Physcomitrella patens subsp. patens
SOURCE Physcomitrella patens subsp. patens
ORGANISM Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
REFERENCE 1 (bases 1 to 567)

AUTHORS

Nishiyama,T., Fujita,T., Shin-I,T., Seki,M., Nishide,H., Uchiyama,I., Kamiya,A., Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe,M.

TITLE

Comparative genomes of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: implication for land plant evolution

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)

PUBMED

12808149

COMMENT

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Center for Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshin@genes.nig.ac.jp

A backbone of the vector is basically from pBluescript II (KS), that was in vivo excised from a 1-FLC phase vector (Carninci et al. 2001). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the

vector(5'-ggaagagagagatccacaccttgagagagttttttttttttt-3' was used as a 1st 3' primer, and

5'-ggttctcgagtcgctgttccagacagcgatgactcgagAACGNNNN-3' as 2nd

5'-hairpin primer, giving the following 5' boarder sequence,

AGGCCAATCGCGGAGCTCGAATTCGCGAAGCCG). cDNA insert could be

amplified with conventional T7 and T3 primers. This full-length

cDNA library was generated according to the method described in

Nishiyama et al. (2003).

Protonemata were blended by the POLYTRON, and then cultivated on

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These clones are available from RIKEN Bio Resource Center

(<http://www.brc.riken.go.jp/lab/epd/Eng/index.html>). The database

of Physcomitrella EST clones is available at the PHYSCODbase

(<http://moss.nibb.ac.jp>).

Location/Qualifiers

1..567

/organism="Physcomitrella patens subsp. patens"

/mol_type="mRNA"

/sub_species="patens"

/db_xref="taxon:145481"

/clone="pph30c04"

/issue_type="mixture of chloronemata and young gametophores with 2 to 5 leaves"

/clone_1lb="full length cDNA library, chloronemata and young gametophores"

ORIGIN

Query Match 60.2%; Score 401.4; DB 3; Length 567;
Best Local Similarity 85.0%; Pred. No. 1.2e-109; Mismatches 79; Indels 0; Gaps 0;

Matches 447; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

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112 GTCTGCACATGCTGCGCAAGACTCTTCTGACATGCTCAAGATGAGAACTGGGCG 171
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567 GTCTTGCACATGCGCGGAGACACACTTCTGACATGCTCAAGATGAGAACTGGGCG 508
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172 AACATCAACCAACGCGAGTATCCAGCTCAGAGAGTTGATCAACAGATGAAGTTCA 231
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507 AACATCAACCAACGCGAGTATCCAGCTCAGAGAGTTGATCAACAGATGAAGTTCA 448
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232 AAGCATTCGATCTGGGCGCACAACAATGCTGACGCGGTGAGAGGACTATATGCTA 291
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412 TGGGAACAAGATGATATCCCGTAGCGCTTCTTGAAGCGAGTTGCGGTTCACTTG 471
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Db 267 TTGGCAACAAGATTGACATCCCTTACGCTCCCTCCGAAGTGAATTCGGTACACTCG 208

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Qy 532 TTGAGGTTTTCATGTCGATGATTTGTGGCAAAATGGGGTACGGTGAAGGTTTCAAGTGA 591

Db 147 NTGAGGTTTTCATGTCGATGATTTGTGGCAAAATGGGGTACGGTGAAGGTTTCAAGTGA 88

Qy 592 TGACCCAGTACATCAAGTGAATTTTCTGTGTAAGGAAGAACTTA 637

Db 87 TGACGAGTATATTAATGATTTTTCATATGACAAAGAAAGTAA 42

RESULT 10
LOCUS CN206979
DEFINITION Tort739 Gametophyte rehydration library Tortula ruralis cDNA, mRNA
SEQUENCE.
ACCESSION CN206979
VERSION CN206979.1 GI:46903710
KEYWORDS EST.
SOURCE Tortula ruralis
ORGANISM Tortula ruralis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Dicranidae; Pottiaceae; Pottiaceae; Tortula.
REFERENCE 1 Oliver,M.J., Dowd,S.E., Zaragosa,J., Mauget,S.A. and Payton,P.R.
AUTHORS (bases 1 to 861)
TITLE The rehydration transcriptome of the desiccation-tolerant bryophyte
Tortula ruralis: transcript classification and analysis
JOURNAL BMC Genomics 5 (1), 89 (2004)
PUBMED 15546486
COMMENT Contact: Oliver Melvin J
USDA-ARS
Plant Stress Lab
3810 4th St, Lubbock, TX 79415, USA
Tel: 806-749-5560
Fax: 806-723-5272
Email: moliver@lbrk.ars.usda.gov
PCR Primers
FORWARD: GTTTCCAGCTACGAC
BACKWARD: CAGGAACGCTATGAC.
FEATURES
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Location/Qualifiers
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Salt; Site_2: NoCl"

ORIGIN
Query Match 58.8%; Score 392.4; DB 7; Length 861;
Best Local Similarity 79.8%; Pred. No. 7.2e-107;
Matches 487; Conservative 0; Mismatches 121; Indels 2; Gaps 2;

Qy 25 CTGTGACCATGTTCTTGATGATGTTTAAAGGCTTCTTGCGAGCATAGGGCTGGGC 84

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Qy 85 AGAAGAGGCCAAATCTCTGTTCTGGGCTCTGCAAAATGCTGGCAAGACTTCTTCTGC 144

Db 224 AGAAGAGGCCAAATCTCTGTTCTGGGCTCTGCAAAATGCTGGCAAGACTTCTTCTGC 283

Qy 145 ACATGCTCAAGATGAAATCTGGGGCAACATCAACCAAGCAATCAACGTCAGAGG 204

Db 284 ACATGCTCAAGATGAAATCTGGGGCAACATCAACCAAGCAATCAACGTCAGAGG 343

Qy 205 AGTTGATATCAACAGAGTGAAGTTCAAGGATTCGATTCGGTGGCCACATCGCTC 264

Db 344 AGCTGACATCAACAGAGTGAAGTTCAAGGATTCGATTCGGTGGCCACATCGCTC 403

Qy 265 GACCGCTGAGAGGACTACTATGCTAAGTGAATGCTATAGTATCTCTGAGAGCAG 324

Db 404 GCGCTGTGTGAGAGACTATTTATGCAAGGTGATGCAATGCTACTCTGTGAGACCCC 463

Qy 325 TAGACAGGAGAGATTGCTGAGTCAAGAAAGAGCTCGATTCTCTCTCCGACGATT 384

Db 464 TAGACAGGAGAGATTGCTGAGTCAAGAAAGAGCTCGATTCTCTCTCCGACGACA 523

Qy 385 CTCTGCCCAAGTTCTGTGCTGCTGCTGCTGCGAAACAAAGATTGATATCCGTACGTTCTT 444

Db 524 CTCTGCCCAAGTTCTGTGCTGCTGCTGCGAAACAAAGATTGATATCCGTATGCGGCT 583

Qy 445 CTGAAGACAGATTGCGGTTACACTTGGGTTGACCATGACCACTGGTAAAGAACGTGA 504

Db 584 CTGAGAGAGAGCTGCGGTATTTCTTGGGCTGACCATGACCAAGGCAATGGAACCTGGA 643

Qy 505 ACCTGGGAGATGACCAATTCGCGCCATTGAGGTTTCAATGTCAGATTTGTGGCAAAA 564

Db 644 ACCTGGGAGATGACCAATTCGCGCCATTGAGGTTTCAATGTCAGATTTGTGGCAAAA 703

Qy 565 TGGGATGAGTGAAGTTTCAAGTGAATGACCCAGTACATCAAGTGAATTTTCTGTG 624

Db 704 TGGGATGAGTGAAGTGAAGTGAATGACCCAGTACATCAAGTGAATTTTCTGTG 761

Qy 625 AAGAGGAAAC 634

Db 762 CATGTAGAAC 771

RESULT 11
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DEFINITION BU595842 normalized full length cDNA library, chloronemata,
caulonemata and rhizoid-like protonemata Physcomitrella patens
subsp. patens cDNA clone pphn10e13 3', mRNA sequence.
BU595842
ACCESSION BU595842.1 GI:37837834
VERSION BU595842.1
KEYWORDS EST.
SOURCE Physcomitrella patens subsp. patens
ORGANISM Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
REFERENCE 1 (bases 1 to 600)
AUTHORS Nishiyama,T., Fujita,T., Shin-i,T., Seki,M., Nishide,H.,
Uchiyama,I., Kamiya,A., Carninci,P., Hayashizaki,Y., Shinozaki,K.,
Kohara,Y. and Hasebe,M.
TITLE Comparative genomics of Physcomitrella patens gametophytic
transcriptome and Arabidopsis thaliana: implication for land plant
evolution
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
PUBMED 12808149
COMMENT Contact: Tadao Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
A backbone of the vector is basically from pBluescript II (KS),
that was in vivo excised from a 1-FLC phase vector (Carninci et al.,
2001). 5' end of the cDNA that was digested with XhoI was ligated
to SalI site of the vector and the 3' end including polyA tail was
vector(5'- GAGAGAGAGAGATCAACCTGAGAGATTTTATTTTATTTTATTTTATTTT-3' was
used as a 1st 3' primer, and
5'-gggttcgagatgctgctgttcacagacagcgtgactcgagacggnnnn-3' as 2nd
5'-hairpin primer, giving the following 5' boarder sequence,
AGGCCAAATCGGCGGACCTCGAATTCGTGAGAGACCG). cDNA insert could be
amplified with conventional T7 and T3 primers. This full-length
cDNA library was generated according to the method described in
Nishiyama et al. (2003).
Protonemata were blended by the POLYTRON, and then cultivated on
the BCDMG medium for 13- 14 days under the continuous light.

QY 524 TCGGCCATTGAGTTTCATGTCAGTATGTCGCAAAATGGGGTACGGTGAAGTTT 583
 Db 205 CCGGCCATTGAGTTTCATGTCAGTATGTCGCAAAATGGGGTACGGTGAAGTTT 146
 QY 584 CAAGTGATGATGACCAAGTACATCAAGTATGTTTCTGTGGAAGAGAACTTA 637
 Db 145 CAAGTGATGATGACCAAGTATGATTAATGATTTGTCATAGACAGAGAAAGTAA 92

RESULT 13
 B9941869 684 bp mRNA linear EST 13-JUN-2005
 LOCUS B9941869 phpf full-length cDNA library Physcomitrella patens subsp.
 DEFINITION patens cDNA clone phpf16p22 5', mRNA sequence.
 B9941869
 VERSION B9941869.1 GI:67569045
 KEYWORDS EST.
 SOURCE Physcomitrella patens subsp. patens
 ORGANISM Physcomitrella patens subsp. patens
 Eukaryota; Viridiplantae; Streptophyta; Bryophyta;
 Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
 1 (bases 1 to 684)
 Fujita, T., Nishiyama, T., Shin-i, T., Kohara, Y. and Hasebe, M.
 Physcomitrella patens EST at a stage of the first asymmetric cell
 division of protoplasts
 Unpublished (2005)
 Contact: Tadashi Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp
 Protoplasts were inoculated on BODAN medium for every ca. 5 days.
 Protoplasts were isolated from the protoneuma, further incubated
 at 25C under continuous light for 2-3 days. The regenerated cells,
 which were rich in cells at a stage during the first asymmetric
 cell division, were collected. Total RNA was extracted for
 constructing a full-length cDNA library. The database of the EST
 clones is available at the PHYSCbase (http://moss.nibb.ac.jp).
 Location/Qualifiers
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 every ca. 5 days. Protoplasts were isolated from the
 protonemata, further incubated at 25C under continuous
 light for 2-3 days. The regenerated cells, which were rich
 in cells at a stage during the first asymmetric cell
 division, were collected. Total RNA was extracted for
 constructing a full-length cDNA library."

ORIGIN
 Query Match 51.8%; Score 345.8; DB 3; Length 684;
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QY 125 TGGCAAGACTACTCTTCTGCAATGCTCAAGATGAGAAACTGGGGCAATCAACCAAC 184
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 QY 305 AGCTATCTCTGTCGACGCGATGACAGGAGAGATTTGCTGACTCAAAAGAGCTGCA 364
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 QY 365 TTCTCTTCTGTCGACGATTTCTGTGCCAAGTCTGTGCTGCTCTGGAGAAACAAGAT 424
 Db 600 CTCTCTGCTCTGCGATGATGCTGCTCTCCCAAGTGTGTGCTGTCTTGTGCAACAAGAT 659
 QY 425 TGATATCCGTAACGCTTCTTGTGAA 449
 Db 660 TGACATCCCTTAAGCTGCGCTCGAA 684

RESULT 14
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 DEFINITION mRNA sequence.
 CK748609
 VERSION CK748609.1 GI:42639032
 KEYWORDS EST.
 SOURCE Persea americana (avocado)
 ORGANISM Persea americana

REFERENCE
 AUTHORS 1 (bases 1 to 751)
 dePamphilis, C., Carlson, J., Ma, H., Soltis, D., Soltis, P.,
 Oppenheimer, D., Frohlich, M., Doyle, J., Tanksey, S., Webb, M.,
 Leebens-Mack, J., Landherr, L., Ilut, D. and Wall, K.
 Generation of ESTs from early flower buds of *Persea americana*
 Unpublished (2003)
 Contact: Claude dePamphilis or James Leebens-Mack
 Mueller Laboratory
 Penn State University
 208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
 State University, University Park, PA 16802, USA
 Tel: 814 863 6413
 Fax: 814 865 9131
 Email: cwdi@psu.edu or jhl10@psu.edu
 The sequence provided is trimmed of vector and low quality regions.
 Full sequence and original trace file are available from the Plant
 Genome Network website (http://Pgn.cornell.edu)
 Plate: pam01-5mnl row: b column: 07
 Seq primer: M13P.

FEATURES
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 Site 2: XhoI. This is a directionally cloned,
 non-normalized library. This library has been generated by
 the Floral Genome Project (FGP). The Floral Genome Project
 is funded by NSF's Plant Genome Research Program

(DBI-0115684). More information about the project can be
obtained at <http://Egfp.bio.psu.edu>

ORIGIN

Query Match 51.4%; Score 343; DB 7; Length 751;
Best Local Similarity 71.5%; Pred. No. 5,8e-92;
Matches 464; Conservative 0; Mismatches 182; Indels 3; Gaps 1;

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QY 538 TTTTCATGTGCAATATTGTGCGCAAAATGGGATACGTTGAAGTTTCAAGTGAATGCC 597
DB 624 TTTNCATGTGCAAGATTTGCTGCGCAAGATGGGTTATGCTGATGGCTTCAAGTGGCTCTC 683
QY 598 AGTACATCAAGTATGTTTTCCTGTGAAGAGGAACTTAGCTCGGTG 646
DB 684 AATACATTAAGTAGGCCGTTGCAACCAAGAAAGATATCCATGTGT 732
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RESULT 15
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ACCESSION BJS72166
VERSION BJS72166.1 GI:27253994
KEYWORDS EST.

SOURCE
ORGANISM Ipomoea nil (Japanese morning glory)

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Solanales; Convolvulaceae; Ipomoeae; Ipomoea.
1 (bases 1 to 749)

TITLE
JOURNAL Hosho, A., Seki, M., Shin-i, T., Carninci, P., Kamiya, A., Shiraki, T.,
Niteesha, E., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S.
ESTs of Japanese morning glory
Unpublished (2002)
CONTACT: Tadasu Shin-i
Center For Genetic Resource Information

National Institute of Genetics
111 Yatae, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tsuhin@genes.nig.ac.jp.
Location/Qualifiers
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FEATURES
source

ORIGIN

Query Match 51.3%; Score 342; DB 3; Length 749;
Best Local Similarity 74.9%; Pred. No. 1.2e-91;
Matches 442; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

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DB 663 AAGAGAGCCAAATCTTGTCTTGGGCTCGACATAGCCGGGAAACACACTTGTCCAT 604
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QY 504 AACCTGGAGATAGCAATTCGCGCCATTTGAGGTTTTCATGTGAGTATGTGCGCAA 563
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DB 183 ATGGGTTATGAGAAAGCTTCAATGATGATGTCATCAATCAATGAATATT 134
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-10-688-481-6

Perfect score: 667

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	667	100.0	667	US-09-828-310-6	Sequence 6, Appl1
2	655	98.2	805	US-09-828-310-1	Sequence 1, Appl1
3	216	32.4	3191	US-09-270-767-13105	Sequence 13105, A
4	209	31.3	716	US-09-533-559-6998	Sequence 6998, Ap
5	179.2	26.9	724	US-08-825-780-2	Sequence 2, Appl1
6	179.2	26.9	1238	US-09-149-476-285	Sequence 285, Ap
7	179.2	26.9	1285	US-09-149-476-146	Sequence 146, Ap
8	174.8	26.2	1700	US-09-533-559-125	Sequence 125, Ap
9	169.8	25.5	903	US-09-016-434-913	Sequence 913, Ap
10	164	24.6	564	US-09-248-796A-6222	Sequence 6222, Ap
11	157	23.5	378	US-09-621-976-458	Sequence 458, Ap
12	117.4	17.6	271	US-09-313-294A-3554	Sequence 3554, Ap
13	115.4	17.3	504	US-09-621-976-445	Sequence 445, Ap
14	95.4	14.3	262	US-09-016-434-501	Sequence 501, Ap
15	92.2	13.8	387	US-09-513-999C-10983	Sequence 10983, A
16	83	12.4	930	US-09-533-559-111	Sequence 111, Ap
17	82.8	12.4	271	US-09-313-294A-3059	Sequence 3059, Ap
18	80.4	12.1	902	US-09-949-016-235	Sequence 235, Ap
19	79.2	11.9	663	US-09-533-559-4386	Sequence 4386, Ap
20	79.2	11.8	895	US-09-949-016-1934	Sequence 1934, Ap
21	78.8	11.8	902	US-09-023-655-1240	Sequence 1240, Ap
22	77.6	11.6	536	US-08-984-550-3	Sequence 3, Appl1
23	77.6	11.6	950	US-08-984-550-1	Sequence 1, Appl1
24	76.2	11.4	550	US-09-359-301A-24	Sequence 24, Appl1

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37	67	10.0	1985	3	US-09-949-016-2434	Sequence 2434, Ap
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39	65.6	9.8	676	3	US-09-533-559-6626	Sequence 6626, Ap
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43	64.2	9.6	400	3	US-09-359-301A-22	Sequence 22, Appl1
44	64.2	9.6	400	3	US-09-771-035A-10	Sequence 10, Appl1
45	63.2	9.5	513	3	US-09-248-796A-6221	Sequence 6221, Ap

ALIGNMENTS

RESULT 1						
US-09-828-310-6						
; Sequence 6, Application US/09828310						
; Patent No. 6689939						
; GENERAL INFORMATION:						
; APPLICANT: COSTA E SILVA, OSWALDO DA						
; APPLICANT: BOHNETT, HANS J.						
; APPLICANT: VAN THIELEN, NOCHA						
; APPLICANT: CHEN, ROUYING						
; TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE						
; FILE REFERENCE: IN PLANTS						
; CURRENT APPLICATION NUMBER: 16313-0039						
; CURRENT FILING DATE: 2001-04-06						
; PRIOR APPLICATION NUMBER: 60/196,001						
; PRIOR FILING DATE: 2000-04-07						
; NUMBER OF SEQ ID NOS: 50						
; SOFTWARE: PatentIn Ver. 2.1						
; SEQ ID NO 6						
; LENGTH: 667						
; TYPE: DNA						
; ORGANISM: Physcomitrella patens						
US-09-828-310-6						
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Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
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Db 661 TTAAAGC 667

RESULT 2

US-09-828-310-1/c
; Sequence 1, Application US/09828310
; Patent No. 6689939
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSMALDO DA
; APPLICANT: BOMBERT, HANS J.
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: 16313-0039
; CURRENT APPLICATION NUMBER: US/09/828,310
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 805
; TYPE: DNA
; ORGANISM: *Physcomitrella patens*
US-09-828-310-1

Query Match 98.2%; Score 655; DB 3; Length 805;
Best Local Similarity 100.0%; Pred. No. 2e-228;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 65 TGCAGCATAGAGGCTGTGCGAAGAGGCCAAATCCGTTTCTGGGTTCTGCATGCG 124
|
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|
Db 721 TGCAGCATAGAGGCTGTGCGAAGAGGCCAAATCCGTTTCTGGGTTCTGCATGCG 662
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|
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QY 125 TGGCAAGACTACTCTTCTGCAATGCTCAAGATGAGAACTGGGGCAACATCAACCAAC 184
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|
|
Db 661 TGGCAAGACTACTCTTCTGCAATGCTCAAGATGAGAACTGGGGCAACATCAACCAAC 602
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|
QY 185 GCATATTCACACGTCAGAGAGGTTGAGTATCAACAGATGAAGTTCAAAGATTCGATCT 244
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Db 601 GCATATTCACACGTCAGAGAGGTTGAGTATCAACAGATGAAGTTCAAAGATTCGATCT 542

QY 245 GGGTGGCCACACATGCTGACGCGGTGAGGAGCTACATATGCTAAGGTGATGCTAT 304
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Db 541 GGGTGGCCACACATGCTGACGCGGTGAGGAGCTACATATGCTAAGGTGATGCTAT 482
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QY 305 AGTGTATCTTCGTGACGCGAGTAGACAGAGGAGATTGCTGAGTCAAGAAAGAGCTGCA 364
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|
Db 481 AGTGTATCTTCGTGACGCGAGTAGACAGAGGAGATTGCTGAGTCAAGAAAGAGCTGCA 422
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QY 365 TTCTCTCTCTCGACGAGATTCTCTGCCAAGTTCTGTGCTGCTGCTGGAAACAAGAT 424
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Db 421 TTCTCTCTCTCGACGAGATTCTCTGCCAAGTTCTGTGCTGCTGCTGGAAACAAGAT 362
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QY 425 TGAATATCCGTACGCTTCTTCTGAGACGAGTTGCGGTTCAACTTGGGTTGACATGAC 484
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QY 485 CACTGTAAAGAACGCTGAACCTGGGAGATAGCAACATTCGGCCATTGAGGTTTCAAT 544
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Db 301 CACTGTAAAGAACGCTGAACCTGGGAGATAGCAACATTCGGCCATTGAGGTTTCAAT 242
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Db 241 GTGCAGTATTTGCGCAAAATGGGGTACCGGTGAAGTTTCAAGTGAATGACCCAGTACAT 182
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QY 605 CAAGTATTTGTTTCTCTGTGAAGAGAACTTAGCTCGGTGTTTAAGACGACGA 659
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Db 181 CAAGTATTTGTTTCTCTGTGAAGAGAACTTAGCTCGGTGTTTAAGACGACGA 127

RESULT 3

US-09-270-767-13105
; Sequence 13105, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13105
; LENGTH: 3191
; TYPE: DNA
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-13105

Query Match 32.4%; Score 216; DB 3; Length 3191;
Best Local Similarity 61.8%; Pred. No. 1.7e-67;
Matches 361; Conservative 0; Mismatches 220; Indels 3; Gaps 1;

QY 33 ATGTTCTGTAGATGTGTTTAAAGGCTTCTTTCGAGCATAGGGCTGTGGCAAGAG 92
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Db 174 ATGTTCTGTAGATGTGTTTAAAGGCTTCTTTCGAGCATAGGGCTGTGGCAAGAG 233
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|
QY 93 GCCAAATCTGTTTCTGGGTTCTGCACAAATGCTGCAAGACTTCTTCTGCATGCTC 152
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|
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Db 234 GCGAAATATATGTTCTGCGGCTCGAATATGCTGGCAAAACCACTTTGCAATGCTC 293
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QY 153 AAGATGAGAACTGGGGCAACATCAACGACGATATCAACGTCAGAGAGTTGAGT 212
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Db 294 AAGATGATAGCTGGCGACATGCGCACACTGCATCAACATCCAGAGGCTGTCC 353
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|
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QY 213 ATCAACAGATGAAGTTCAAGATTCGATCTGGGTGGCAACATTCGTCGACGCG 272
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|
|
Db 354 ATGGAACATGCGCTTCACTACATTCGACTTGGGTGGCAACATTCGTCGACGCG 413
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|
|
QY 273 TGAAGGACTACTATCTAAGGTGATGCTATATGCTATCTCGTCGACGAGTAGACAG 312
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|
Db 414 TGAAGGACTACTCTTCTGCTGTGAGCGCATGCTTTCTTAATTAACGCTGGACCGT 473
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|
|
QY 333 GAGAGATTTGCTGATCAAGAAAGAGCTCGATTTCTTCTCTCGACGATTCCTGCTC 392

Db 474 GGGCGCTTCAGAGAGAGCAAAACGAGCTGATTCCTGCTCAAGATAGAGGCGTGTCC 533
Qy 393 CAAATTCCTGTGTCTCTCTCGGAAACAAAGATTGATATCCCGTACCGCTTCTTCTGAAGC 452
Db 534 AACTGCCCGGTGTCTATTATTTGGCAACAAATCGATTAGCCCGCGGCTGTAGCGGAGT 593
Qy 453 GAGTTGCGGTTCACACTTGG--GTTGACCATGACCATGTGTAAAGAAAGGTGAACCTG 509
Db 594 GAGCTAGAAAGCTGTTCGACCTGTATCACTAAACCGGCAAGGCAAGGCAAGTTGACACC 653
Qy 510 GGAGATAGCAACATTCGGCCCATTTGAGTTTCATGTGCAATTTGTGCGCAAAATGGGG 569
Db 654 GCGGATTTGCGCGCGCGTCTCTGGAATTGTTCATGTGCTCCGCTGCAAGCAGAGGGG 713
Qy 570 TACGGTGAAGTTTCAAGTGAATGATGACCCAGTATCAATGATTT 613
Db 714 TACGGCGAGGTTTCCGTTGGCTGTGGCGCAGTATATGATTTAACT 757

RESULT 4

US-09-533-559-6998
; Sequence 6998, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjaerke Olsen
; TITLE OF INVENTION: Methods for Monitoring Multiple Gene
; FILE REFERENCE: Expression
; FILE REFERENCE: 5849,200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ. ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ. ID NO 6998
; LENGTH: 716
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
US-09-533-559-6998

Query Match 31.3%; Score 209; DB 3; Length 716;
Best Local Similarity 61.6%; Pred. No. 2.2e-65;
Matches 354; Conservative 0; Mismatches 215; Indels 6; Gaps 1;

Qy 30 ACCATGTTTCTTGTAGATTGTTTACGGCTTCTTCTGCGAGCATAGGGCTGTGGCAGAAG 89
Db 92 ACCATGTGATCATTTAACTGTTCTACGAGTCTCTGCTCCCTCGGCTGTCTCAACAAG 151
Qy 90 GAGGCCAAATCTGTTTCTGGGTCTGCAATGTGCGAAGACTACTCTTCTGCAATG 149
Db 152 CAGGCCAGCTCTCTCTCTGCGCTTGAACAATGCCGAAAGACAGCCCTTCTGCAATG 211
Qy 150 CTCAGAGATGAGAACTGGGGCAACATCAACGAGTATCCAAAGTCCAGAGAGTTG 209
Db 212 TTGAAGAAGACCGGGGTGTGCGTTCTTCAAGCCAGCTCATCGAGTGGAGAGCTC 271
Qy 210 AGTATCAACAGAGTGAAGTTCAAGCATTCGATCTGGGTGGCCACACAAATGCTCGAGC 269
Db 272 GCTATCGAAACAACCCCTTCACTACCTTGAAGCTGGGTGTGACACGAGCGCCGACGT 331
Qy 270 GTGTGAGGAGACTACTATGCTAAGGTGATGATAGTATCTCGTCAAGAGTAC 329
Db 332 CTCTGGAAGACTATTTCTCCGAGAGTACGGTATCGTTTCTCTGTTAGCCCAAGGAC 391
Qy 330 AGGAGAGATTTGCTGAGTCAAGAAAGAGCTCGATTCTTCTCTCCAGATTCTCTG 389
Db 392 CAGAGAGTTTCCCGAGTCCAAAGCGGAGAGTGAAGCTCTCTCTGCGCATGAGAGACTC 451

Qy 390 TCCAGTTCTCTGTCTGTCTGCTCTGGAACAAAGATTGATATCCCTGACTTCTTCTGAA 449
Db 452 GCGAAGTCTCCCTTCTCTATTTCTGGCAACAAAGATGACACCCGAGCGCTGACGAG 511
Qy 450 GAGGAGTTGCGGTTCACACTTGGGTTAACATGACCACTGTGTAAAGAAAGGTGAACCTG 509
Db 512 GACGAAGTGAAGACACAGCTGGGACTTACAGACCAAGAAAGGCAAGGTGCCACTT 571
Qy 510 GGAGATAGCAACATTCGGCCCATTTGAGTTTTCATGTGAGTATTTGTGCGCAAAATGGGG 569
Db 572 GAGG-----GCATCGAACCGATCGAGTCTTCATGTGAGTGTGTGATGACAGGCT 625
Qy 570 TACGGTGAAGTTTCAAGTGAATGATGACCCAGTATCAT 604
Db 626 TACGGCGAGGTTATCAAGTGTGCTGTCCCAATTCGT 660

RESULT 5

US-08-825-780-2
; Sequence 2, Application US/08825780
; Patent No. 5834238
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NOVEL HUMAN GTP BINDING P
; TITLE OF INVENTION: ROTHEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,780
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0264 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ. ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 724 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BESTTUT14
; CLONE: 2742252
US-08-825-780-2

Query Match 26.9%; Score 179.2; DB 2; Length 724;
Best Local Similarity 58.5%; Pred. No. 1.8e-54;
Matches 332; Conservative 0; Mismatches 233; Indels 3; Gaps 1;

Qy 47 TTGGTTTACGGCTTCTTCTGCGATTAAGGCTGTGGCAAGAGAGGCCAAATCTCTGT 106
Db 82 TGGTTTACAGAGTGTGCTACAGTTTATAGATTATATAGAAACTGTAACTGTGATT 141

QY 107 TCTGGGTCTGCACATGCTGGCAAGACTACTCTTCTGACATGCTCAAGATGAAACT 166
Db 142 TCTGGATTTGATATGATGAGGAAACAACTTCTCACTGCTAAAGATGACACT 201
QY 167 GGGGCAATCATCAACGCAAGTATCCAAAGCTGAGAGTGTAGTCAACAGAGGAA 226
Db 202 TGGACAACTATCTCCAACTTACATCCACTTCCGAAAGTACCACTTGTGCGATGAC 261
QY 227 GTTCAAGACATTCATCTGGGTGGCCACAACTGCTGACGCGTGTGAGGAGCTACTA 286
Db 262 GTTTACAACTTTTATCTGGGTGACATGTTCAAGCTCGAAAGATGTGAAAACTACTCT 321
QY 287 TGTCAAGTGTATCTATAGTATCTCTGAGACGCGATGACAGGAGAGATTTGCTGA 346
Db 322 TCTGCTATCAATGCACTGTATTTCTGTGATTTGTGACAGACCAAAAGGCTGTAGA 381
QY 347 GTCAAGAAAGAGCTCGATTTCTTCTCTCGACGATTTCTGTCCAAAGTTCTGTGCT 406
Db 382 GTCAAAAGAAACCTTGTATTTACTTAATGACAGATGAAACCTTCTTAATGTGCTTATCT 441
QY 407 CGTCTGGGAAACAAGATTGATATCCGTAACGTTCTTCTGAAAGACGAGTTGCGGTTTAC 466
Db 442 GATTTCTGGGAATTAAGATCGACAGACCTGAAGCCATCAGTGAAGAGGTTGCGAGAGAT 501
QY 467 ACTTGGGT--GACCATGACCATCTGTAAAGAAACGTTAAGTGGAGATGACACAT 523
Db 502 GTTGTGTTATATGTGTCAGACAAAGGAGATATCTCTGAAAGAACTGAATGTC 561
QY 524 TGGGCAATGAGGTTTTCATGTGACATGTTGCGGAAATGGGGTACCGTGAAGGTTT 583
Db 562 CCGACCTTGAAGATTTTCAATGTGTATGTCTCAAAAGCAAGATTACGAGAGGCTT 621
QY 584 CAAGTGATGACCAAGTACATCAAGTGA 611
Db 622 CCGCTGATGCGACAGTACATGATTAA 649

RESULT 6
US-09-149-476-285
Sequence 285, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/047,613
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EARLIER APPLICATION NUMBER: 60/047,612
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EARLIER APPLICATION NUMBER: 60/043,601
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,580
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EARLIER FILING DATE: 1997-04-11
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EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/056,889
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EARLIER APPLICATION NUMBER: 60/056,893
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EARLIER APPLICATION NUMBER: 60/056,630
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EARLIER APPLICATION NUMBER: 60/056,662

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EARLIER APPLICATION NUMBER: 60/056,872
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EARLIER APPLICATION NUMBER: 60/056,864
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EARLIER FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/056,875
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EARLIER APPLICATION NUMBER: 60/056,862
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EARLIER APPLICATION NUMBER: 60/057,650
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EARLIER APPLICATION NUMBER: 60/056,884
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EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 26.9%; Score 179.2; DB 3; Length 1228;
Best Local Similarity 58.5%; Pred. No. 2.5e-54;
Matches 332; Conservative 0; Mismatches 233; Indels 3; Gaps 1;

QY 47 TTGGTTTACGGCTTCTTCGAGCATAGGGCTGTGCGAAGAGGCCCAATCCTGTT 106
DB 118 TGGTTTACGACATGTCCTTCACTTTTATAGATTATATAGAAACGTGTAATCTGTTAT 177
QY 107 TCTGGTCTCGACAACTGTGCGAAGCTACTCTTCTGACATGCTTCAGAGTGAACCT 166
DB 178 TCTGGATTGATTAATGACGAAAAACAATTTGCTACACATGCTTAAAGATGACGACT 237
QY 167 GGGGCAACATCAACCAACCATATCCACGTCAGAGGTTGATATCAACAGTGA 226
DB 238 TGGACAACTGTCCTCAACATTAATCCATTCCTCCAGAACTGACCATTTCTGATGAC 297
QY 227 GTTCAAGCATTCGATCTGGTGTGCGACACAATTCGTCAGCCGTTGTGAGGAGCTACTTA 286
DB 298 GTTTACACCTTTTGTGATCTGGTGTGACATGTTCAAGTGTGAAGAGTGTGAAAACTACCT 357
QY 287 TGTAAAGTGATGCTATAGTATCTGTCGACGAGTAGACAGGAGAGATTGCTGA 346
DB 358 TCTGTATCAATGAGCATTTGATTTCTGTGATTTGTGACACACGAAAGCTGTAGA 417
QY 347 GTCAAGAAAGAGCTGATTTCTTCTCCGACGATTTCTGTCCAAAGTCTCTGTGCT 406
DB 418 GTCAAGAAAGAGCTGATTTCTTCTCCGACGATTTCTGTCCAAAGTCTCTGTGCT 477
QY 407 CGTCCCTGGGAAACAAGATTGATATCCGTAAGCTTCTTGAAGACGAGTTGGGTTAC 466
DB 478 GATCTTGGGAATATAGATGACAGACCTTGAAGCATCACTGAAGAGAGTTGGAGAGAT 537
QY 467 ACTTGGTT---GACCATGACCACTGTGTAAGAAACGTTGAACCTGGAGATAGCAACAT 523
DB 538 GTTTGTTTATATGTCAGACAAACAGAAAGGAGTATATCTGTAAAGAACTGAATGC 597
QY 524 TGGGCCCATTTAGAGTTTTCATGTGCAATTTGTGCGCAAAATGGGGTACGGTGAAGTTT 583
DB 598 CCGACCTTAAGAAAGTTTTCATGTGTGTGCTCAAAAGAACAAAGGTTTACGGAGAGGCTT 657
QY 584 CAAAGTATGACCCAGTACATCAAGTGA 611
DB 658 CCGCTGATGACACAGTACATTTGATTAA 685

RESULT 7
US-09-149-476-146
Sequence 146, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins

[illegible]


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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
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; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
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; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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Query Match      26.9%; Score 179.2; DB 3; Length 1285;
Best Local Similarity 58.5%; Pred. No. 2.6e-54;
Matches 332; Conservative 0; Mismatches 233; Indels 3; Gaps 1;

QY 47 TTGGTTTACGGCTTTCTTCGAGCATAGGCGTGTGCGAAGAGGCAAAATCCGTT 106
DB 145 TGGTTTACGAGCTGTCTTACAGTTTATGAGATTTATTAAGAAACTGTAACTGATTT 204
QY 107 TCTGGGTCTCGACATGCTGGCAGACACTCTTCTTCGACATGTCTCAAGATGAGAACT 166
DB 205 TCTTGGATTGGATTAATGACGAGAAAAACAATTGCTACATGCTTAATAAATGACAGACT 264
QY 167 GGGGCAACATCAACCAACGAGATTCACAGCTCAGAGAGTGAATTCACAGATGAA 226
DB 265 TGGCAACATGTCCTCAACATTCACCTCCGAACTGCAAGAACTGACCTCTGCACTGAC 324
QY 227 GTTCAAGCATGATGATCTGGGTGGCCACACATGCTCGACGGGTGAGAGGACTACTA 286
DB 325 GTTTACAACCTTTTATCTGGGTGAGACATGTTCAAGCTCGAAGAGTGGAAAACTACTCT 384
QY 287 TGCTAAGGTGATGCTAATGATGATCTCTCGACGCGAGTACAGGAGAGATTTGCTGA 346
DB 385 TCTGCTATCAATGAGCATTTGATTTCTGGTGGATTTGTCAGACCAAGAAAGGCTTTAGA 444

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QY 347 GTCAAGAAAGAGCTCGATTTCTTCTCTCCAGCATTTCTGTCCAAATTCTGTGCT 406
DB 445 GTCAAAAGAAAGACTGATTTACTATGACATGAAACCATTTGCTAATGCTCTACT 504
QY 407 CGTCTGGGAAACAAGATGATATCCCGTCTTCTTGAAGAGAGTTCGGTTAC 466
DB 505 GATTTCTGGGAAATTAAGATCGACGACCTGAAACCATCACTGAGAGAGTTCGAGAGAT 564
QY 467 ACTGGGTGACCAT---GACCACTGGTAAAGAAACGGTGAACCTGGAGATAGCAACT 523
DB 565 GTTTGTTTATATGTCACACACAGAAAGGGAGTATATCTTGAAGAACTGATATC 624
QY 524 TCGGCCATTGAGTTTTCATGTGCAATTTGCGCAAAATGGGGTACGTTGAAGTTT 583
DB 625 CCGACCTTGAAGAGTTTTCATGTGATGCTGCAAAAGCAAGGTTGAGGAAGGCTT 684
QY 584 CAATGATGATCCACGATCATCAAGTGA 611
DB 685 CCGCTGATGCGACAGTACATGATTTAA 712

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RESULT 8
US-09-533-559-125
; Sequence 125, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Key
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 1700
; TYPE: DNA
; ORGANISM: Fusarium venenatum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1700)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-125

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Query Match      26.2%; Score 174.8; DB 3; Length 1700;
Best Local Similarity 60.7%; Pred. No. 1.3e-52;
Matches 320; Conservative 0; Mismatches 200; Indels 7; Gaps 2;

QY 30 ACCATTTTCTGTGATTTGTTTACGCTTTCTTCGACATATGGGCTGTGCGAAG 89
DB 109 ATCATGTGATGTCAACATGTTTCTAGATGTGCTGTCTCTCGGCTGCTCAACAG 168
QY 90 GAGGCCAAATCTGTTTCTGGGTCTCGACAATGTGCGAAGCTACTTCTGACATG 149
DB 169 CACGCAAGCTGTTTCTCGGTCTTGACMAAGCCGGAAGACTACTTCTCCACATG 228
QY 150 CTCAGATGAGAAACTGGGGCAACATCAACCAACGACATTCACAGTCAAGAGTTG 209
DB 229 CTGAAGACGACGATGTTCATTCAGCCCACTTCACCCCAATCCAGNAGCTT 288
QY 210 AGTATCAACAGATGAAGTTCAAGATTCGATGTGGGTGGCCACACATCGTCAGCG 269
DB 289 GCTATTGTGAAGCTCGCTTCAACACTTTCGATCTTGGTGGCATTCACAGGCGGAGCT 348
QY 270 GTGTGAGGAGACTATATCTAAGGTGATGTATATGATATCTGTGACGACGATGAG 329

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Db	349	ATCTGGGGCGCATTTACTTCCCCGACGTCACAGGTCGTCTTCTCTTATGACGGCCACAAGAC	408
Qy	330	AGGAGAGATTTTGTCTGATGTCAAAGAAAGTCGATTCCTTCTCTCCGAGATTTCTG	387
Db	409	CACAGAGATTGTGTATGTATGCTAAAGGCGAGCTGACAGCCCTCTCTCTATGAGAAACTT	466
Qy	390	TCCCAAGTTCCTGTGCTGCTGCTGGAAACAAGATTGATATCCGTACGCTTCTTCTGAA	445
Db	469	TCCAAAGTTCCTTGTGTGATCTCCGCGAACAAAGATGACACACCCG-ATGCGGTCTCCGAA	527
Qy	450	GACAGTGTGGGCTTCACTGTGGGTGACATGATGCATCGTGTAAAGAAAGGTGAACCTG	507
Db	528	GAGCAATGTGGACCAACACTCGGCGCTCTACCAAAACAACCGTAAAGGCAAGGTCACATT	587
Qy	510	GGAGATGCAACAATTGGGCGCCATTGATAGTTTCAATGTGCAAGTATGT	556
Db	588	GAGG-----GCATCGACCTATTGAGCTCTTTCATATGTGTCANTATGT	628

RESULT 9
US-09-016-434-913
; Sequence 913, Application US/09016434

```

1  GENERAL INFORMATION:
2  APPLICANT: Janice Au-Young
3  APPLICANT: Jeffrey J. Sellhammer
4  TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
5  TITLE OF INVENTION: PATHWAY GENE EXPRESSION
6  NUMBER OF SEQUENCES: 1490
7  CORRESPONDENCE ADDRESS:
8  ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
9  STREET: 3174 PORTER DRIVE
10 CITY: PALO ALTO
11 STATE: CALIFORNIA
12 COUNTRY: USA
13 ZIP: 94304
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/09/016,434
21 FILING DATE: HERMITH
22 CLASSIFICATION:
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER:
25 FILING DATE:
26 CLASSIFICATION:
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Zeller, Karen J.
29 REGISTRATION NUMBER: 37,071
30 REFERENCE/DOCKET NUMBER: PA-0002 US
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: (650) 845-0555
33 TELEFAX: (650) 845-4166
34 INFORMATION FOR SEQ ID NO: 913:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 903 base pairs
37 TYPE: nucleic acid
38 STRANDEDNESS: single
39 TOPOLOGY: linear
40 IMMEDIATE SOURCE:
41 LIBRARY: TONSNOT01
42 CLONE: 735249
43 US-09-016-434-913

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Query Match	25.5%	Score 169.8	DB 3	length 903
Best Local Similarity	58.4%	Pred. No.5,6e-51		
Matches 316; Conservative	0	Mismatches 222	Indels 3	Gaps 1
46	ATTGGTTTACCGCTTTCTTGGAGACATAGGGCTGTGGCAGAAAGAGGCCAAATTCCTGT	105		

Db	237	ATGGCTTAGCAGATGTGCTCCAGTTCTTAGAGACTGTACAAAGAAATCTGGAAAATTCTGTAT	296
Qy	106	TTCTGGGCTTCGACATAGCTGCGAAGACTACTCTTTCTGACATGCTCCAGAGATGAGAAAC	165
Db	297	TCTTAGGTTTGGATTAATGACAGGCAAAACCACTTCTTCCACATGCTCCAAAGATGACAGAT	356
Qy	166	TGGGGCAATCAACCAACGCGAGTATCCAAAGTCAGAGGAGTGAAGTATCAACAGAGTGA	225
Db	357	TGGCGCAACATGTTCCAACTACATCCGACATCGAAGAGCTAACATTTCTCGAATGA	416
Qy	226	AGTTCAAGCATTCGATCTGGGTGGCCACACATGCTCGACGCGTGTGAGGAGACTACT	285
Db	417	CCTTACAACTTTTATCTTGGTGGGACGACGAACAGCAGTCCGCTTTGGAAAAATTATATC	476
Qy	286	ATGCTAAGTGGATGCTATAGTGTAATCTGCTGAGCGCAGATAGCAAGGAGAGATTGCTG	345
Db	477	TCCACGACATTAATGGAGATTGTCTTCTGTGGACCTGTGCAAGTCAATTCCTGCGCTCGTGG	536
Qy	346	AGTCAAAGAAAGAGCTCGATTCCTCTCTCTCGACGATTCCTGTGCCAAGTCTGTGTC	405
Db	537	AATCCAAAGTTAGGCTTAATGCTTTAATGATGATGATGAACAAATATCCAAATGTGCAATCC	596
Qy	406	TCGTCCTGGGAAAACAAGATTGATATCCGTAAGCTTCTTCTGAAGACGAATTGGCGTTCA	465
Db	597	TTATCTTGGGTAAACAAAATTGACAGAACAGATGCAATCAGTGAAGAAAACTCCGTGAGA	656
Qy	466	CACCTGGGTTGACCAT--GACCACTGTGTAAGAAACGGTGAACCTGGAGATAGCAACA	522
Db	657	TATTTTGGGCTTATAGACAGACCAACAGAAAGGGGAATGTGACCTGTAAAGAGCTGAATG	716
Qy	523	TTGCGCCATTGAGGTTTTCATGTGCAAGTATTTGTGCGCAAAATGGGGTACGGTGAAGGTT	582
Db	717	CTGCGCCCATGGAAGTGTTCATGTGCAAGTGTCTCAAGAGGCAAGGTTTACGGCGAGGGGT	776
Qy	583	T 583	
Db	777	T 777	

RESULT 10
US-09-248-796A-6222
; Sequence 6222, Application US/09248796A

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: PATENT: NO. 0110
: GENERAL INFORMATION:
: APPLICANT: Keith Weinbock et al
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
: TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 107196.132
: CURRENT APPLICATION NUMBER: US/09/248,796A
: PRIORITY FILING DATE: 1999-02-12
: PRIOR APPLICATION NUMBER: US 60/074,725
: PRIOR FILING DATE: 1998-02-13
: PRIOR APPLICATION NUMBER: US 60/096,409
: PRIOR FILING DATE: 1998-08-13
: NUMBER OF SEQ ID NOS: 28208
: SEQ ID NO 6222
: LENGTH: 564
: TYPE: DNA
: ORGANISM: Candida albicans
: US-09-248-796A-6222

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Query Match	24.6%	Score 164	DB 3	Length 564
Best Local Similarly	58.1%	Pred. No. 5.4e-49		
Matches 309	Conservative 0	Mismatches 220	Indels 3	Gaps 1

QY 73 TAGGGCTGTGCAGGAAGGCGAAAAATCCGTTTCTGGGCTCGACAATCTGGCAGA 132

Db 32 TAGCATTTATGGAATTAACATGCCAAATTATTTATTTTACGGTTAGATATCTCGTAAAA 91

OY 133 CTACTCTTCTGCACATGCTCAAGATGAGAAAATCTGGGCGACATCAACCAACGCAATTC 192

Db 92 CTACTCTTTTACATATGTTTAAAGATGATGATATGGCCACTTTTACACCAACATTTCATC 151

SEQ ID NO 445
LENGTH: 504
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 141..503
US-09-621-976-445

Query Match 17.3%; Score 115.2; DB 3; Length 504;
Best Local Similarity 58.9%; Pred. No. 3.5e-31;
Matches 198; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

QY 46 ATTGTTTACGGCTTTCTTCCGACATAGGGCTGTGGCAAGAGGCCAAATCTCTGT 105
Db 169 ATGGCTTCACAGAGTGCTCCAGTCTCTAGAGACTGTACAGAAATCTGAAAACTGTAT 228
QY 106 TTCTGGGCTTCGACATGCTGGCAAGCTACTCTTCTGACATGCTCAAGATGAGAAAC 165
Db 229 TCTTAGGTTTGGATTAAGCAGGCAAAACACTCTTCTTCAATGCTCAAGATGACAGAT 288
QY 166 TGGGGCAACATCAACCAAGCAGATTCACATCGTCAAGAGGAGTTGATCAACAGAGTGA 225
Db 289 TGGGCCACACATGTTCCACACTACATCCAGATCAGAAAGCTAACATTTGCTGGAATGA 348
QY 226 AGTTCAAGCATTCGATCTGGGTGGCCACCAATCGCTCGACGGGTGAGAGGACTACT 285
Db 349 CCTTACACATTTGATCTTGATGTTGGGACGAGCAAGRCGTGGGTTTGGAAAAATATC 408
QY 286 ATGCTAAGGTGATGCTATGATGATCTCTGACGCAAGTACAGAGGAGATTTCTG 345
Db 409 TCCGAGCAATTAATGGAGATGTTCTTCTGTTGAGATGTCGAGATCATTCCTGCTGTGG 468
QY 346 AGTCAAGAAAGAGCTGATCTCTCTCTCCGACG 381
Db 469 ATCCAAAGTTGAGCTTAATGCTTAATGACTGATG 504

RESULT 14

US-09-016-434-501
Sequence 501, Application US/09016414
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 501:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSNON01
CLONE: 2278736
US-09-016-434-501

Query Match 14.3%; Score 95.4; DB 3; Length 262;
Best Local Similarity 62.2%; Pred. No. 3.8e-24;
Matches 150; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 73 TAGGCTGTGGCAAGAGAGGCCAAATCTGTTTCTGGGTCTCGACATAGCTGGCAAGA 132
Db 21 TAGGATTAATTAAGAAACGTGAACGTGTATTTCTTGATTTGATTAAGCAAGAAAAA 80
QY 133 CTACTCTTTCGACATGCTCAAGATGAGAACTGGGGCAACATCAACAGCAGATATC 192
Db 81 CAACATTTCTACACATGCTTAAGATGACAGATTTGACCAACATGCTCCAACTATATC 140
QY 193 CAACGTCAAGAGAGTTGATGATCAACAGACTGAAGTTCAAGCATTGATCTGGGTGGCC 252
Db 141 CCACTTCGAGAAAGATGACCATGCTGTGATGACGTTTACACTTTTGTGATCTGGGTGAC 200
QY 253 ACACAATGCTGACAGCGGTGTGAGAGGACTACTATGCTAAGGTGATGCTATGCTATC 312
Db 201 ATGTTCAAGCTCAAGAGGTGTGAAAAAATACCTTCTGCTATCAATGCAATGTATTTTC 260
QY 313 T 313
Db 261 T 261

RESULT 15

US-09-513-999C-10983
Sequence 10983, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PATENT NO. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 10983
LENGTH: 587
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc_feature
LOCATION: 426-
OTHER INFORMATION: m=a or c
US-09-513-999C-10983

Query Match 13.8%; Score 92.2; DB 3; Length 587;
Best Local Similarity 65.1%; Pred. No. 9.8e-23;
Matches 136; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 46 ATTGTTTACGGCTTTCTTCCGACATAGGGCTGTGGCAAGAGGCCAAATCTCTGT 105
Db 156 ATGGCTTCACAGAGTGCTCCAGTCTCTAGAGACTGTACAGAAATCTGAAAACTGTAT 215

Qy	106	TTCTGGGCTCTCGACATGCTGGCAAGACTCTTCTGACATGCTCAAGATGAGAAAC	165
Db	216	TCTTAGGTTTGGATTAATGAGGCAAAACACTCTTCTCAATGCTCAAGATGACAGAT	275
Qy	166	TGGGGCAACATCAACCAACGCAAGTATCCAACTGAGAGAGTTGAGTATCAACAGATGA	225
Db	276	TGGGCCAACATGTTCCAACTACATCCGACATCAGAGAGCTAACATTTGCTGGAATGA	335
Qy	226	AGTTCAAAGCATTCGATCTGGGTGGCCAC	254
Db	336	CCTTTAACACTTTTGATCTTGGTGGGCAC	364

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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

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Perfect score: 667
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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
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- 2: /cgn2_6/prodata/1/pubpna/us08_PUBCOMB.seq:*
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- 9: /cgn2_6/prodata/1/pubpna/us10F_PUBCOMB.seq:*
- 10: /cgn2_6/prodata/1/pubpna/us11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	667	100.0	667	3 US-09-828-310-6	Sequence 6, Appl 1
2	667	100.0	667	8 US-10-688-481-6	Sequence 6, Appl 1
3	655	98.2	805	3 US-09-828-310-1	Sequence 1, Appl 1
4	655	98.2	805	8 US-10-688-481-1	Sequence 1, Appl 1
5	349.6	52.4	954	7 US-10-767-701-13805	Sequence 13805, A
6	340.4	51.0	954	7 US-10-425-114-7242	Sequence 7242, Ap
7	340.4	51.0	1221	8 US-10-425-115-143342	Sequence 143342, Ap
8	340.4	51.0	1645	8 US-10-425-115-143343	Sequence 143343, Ap
9	338.4	50.7	1070	8 US-10-425-115-98353	Sequence 98353, A
10	335.6	50.3	955	7 US-10-425-114-21639	Sequence 21639, A
11	332.4	49.8	966	7 US-10-425-114-13536	Sequence 13536, A
12	332.4	49.8	1017	7 US-10-425-114-33380	Sequence 33380, A
13	332.4	49.8	1334	8 US-10-425-115-98354	Sequence 98354, A
14	330.4	49.5	986	7 US-10-425-114-20345	Sequence 20345, A
15	330.4	49.5	1051	7 US-10-425-114-20291	Sequence 20291, A
16	330.4	49.5	1073	7 US-10-425-114-378	Sequence 378, App
17	330.4	49.5	1117	7 US-10-425-114-27102	Sequence 27102, A
18	330.4	49.5	1337	8 US-10-425-115-143340	Sequence 143340, A
19	329.2	49.4	1164	7 US-10-425-114-26805	Sequence 26805, A
20	328.8	49.3	928	7 US-10-767-701-15389	Sequence 15389, A
21	326.2	48.9	1688	7 US-10-437-963-58339	Sequence 58339, A
22	326	48.9	1184	7 US-10-437-963-45082	Sequence 45082, A
23	324	48.6	1036	7 US-10-424-599-31196	Sequence 31196, A

24	321.4	48.2	991	7 US-10-424-599-13515	Sequence 13515, A
25	320	48.0	1303	8 US-10-425-115-143338	Sequence 143338, A
26	319.6	47.9	1191	7 US-10-424-599-139806	Sequence 139806, A
27	318.8	47.8	928	7 US-10-425-114-11886	Sequence 11886, A
28	318.8	47.8	1332	7 US-10-424-599-13513	Sequence 13513, A
29	313	46.9	807	8 US-10-767-795-1302	Sequence 1302, Ap
30	312.8	46.9	994	8 US-10-767-795-1303	Sequence 1303, Ap
31	312.6	46.9	1047	8 US-10-767-795-1304	Sequence 1304, Ap
32	296.6	44.5	592	7 US-10-021-323-15172	Sequence 15172, A
33	295	44.2	675	3 US-09-770-149-378	Sequence 379, App
34	292.2	43.8	811	8 US-10-425-115-140995	Sequence 140995, A
35	288.8	43.3	1164	7 US-10-424-599-32367	Sequence 32367, A
36	283.8	42.5	764	7 US-10-424-599-32368	Sequence 32368, A
37	275	41.2	1066	7 US-10-424-599-142530	Sequence 142530, A
38	272.6	40.9	569	7 US-10-021-323-1674	Sequence 1674, Ap
39	262.8	39.4	603	7 US-10-021-323-11457	Sequence 11457, A
40	262	39.3	570	8 US-10-425-115-12354	Sequence 12354, A
41	220.6	33.1	692	7 US-10-437-963-55941	Sequence 55941, A
42	218.8	32.8	570	5 US-10-128-714-2426	Sequence 2426, Ap
43	216	32.4	992	10 US-11-097-143-15608	Sequence 15608, A
44	215.6	32.3	570	5 US-10-128-714-7426	Sequence 7426, Ap
45	213	31.9	660	7 US-10-437-963-20654	Sequence 20654, A

ALIGNMENTS

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RESULT 1
US-09-828-310-6
; Sequence 6, Application US/09828310
; Patent No. US2002066124A1
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: 16313-0039
; CURRENT APPLICATION NUMBER: US/09/828, 310
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196, 001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 667
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-09-828-310-6

Query Match      100.0%; Score 667; DB 3; Length 667;
Best Local Similarity 100.0%; Pred. No. 2.5e-220;
Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATCCCGGCTCCGATGATACCAAGGCTGATCCATGTTCTTGATGATGTTTACGGCT 60
DB      1 ATCCCGGCTCCGATGATACCAAGGCTGATCCATGTTCTTGATGATGTTTACGGCT 60
QY      61 TTCTTGCGAGCATATGAGGCTGTGCGAGAGAGGCAAAATCCTGTTCTGAGTCTCGACA 120
DB      61 TTCTTGCGAGCATATGAGGCTGTGCGAGAGAGGCAAAATCCTGTTCTGAGTCTCGACA 120
QY      121 ATGCTGCAAGACTACTCTTTGACATGCTCAAGATGAGAAATCGGGCAATCAAC 180
DB      121 ATGCTGCAAGACTACTCTTTGACATGCTCAAGATGAGAAATCGGGCAATCAAC 180
QY      181 CAACGAGATATCCAGTCTGAGAGATTTGATATCAACAGATGATTTCAAGCATTCG 240
DB      181 CAACGAGATATCCAGTCTGAGAGATTTGATATCAACAGATGATTTCAAGCATTCG 240
QY      241 ATCTGGTGGCCACATATGCTGCAAGCGGTGAGGAGACTACTGATGATGATGATG 300
DB      241 ATCTGGTGGCCACATATGCTGCAAGCGGTGAGGAGACTACTGATGATGATGATG 300
```


Db 241 ATCTGGGTGGCCACACATGCTTCGACGCGTGTGGAGGAACTATCTATGTAAAGTGTATG 300
Qy 301 CTATAGTATCTCTGTCGACGAGTATGACAGGAGAGATTTGCTGAGTCAAAAGAGAGC 360
Db 301 CTATAGTATCTCTGTCGACGAGTATGACAGGAGAGATTTGCTGAGTCAAAAGAGAGC 360
Qy 361 TCGATTCTCTCTCTCGGAGATTTCTGTGCCAAGTTCTGTGCTGCTGCTGGAAACA 420
Db 361 TCGATTCTCTCTCTCGGAGATTTCTGTGCCAAGTTCTGTGCTGCTGCTGGAAACA 420
Qy 421 AGATTGATATCCCGTACGCTTCTTGAAGAGGTTGGGTTCCACTTGGGTTGACA 480
Db 421 AGATTGATATCCCGTACGCTTCTTGAAGAGGTTGGGTTCCACTTGGGTTGACA 480
Qy 481 TGACCACTGGTAAAGAAAGGAGTGAACCTGGAGATGACCAATTCGGCCCATTTGAGTTT 540
Db 481 TGACCACTGGTAAAGAAAGGAGTGAACCTGGAGATGACCAATTCGGCCCATTTGAGTTT 540
Qy 541 TCATGTGCAATGATTTGTGCGCAAAATGGGGTACGGTGAAGGTTTCAAGTGAATGACCAAGT 600
Db 541 TCATGTGCAATGATTTGTGCGCAAAATGGGGTACGGTGAAGGTTTCAAGTGAATGACCAAGT 600
Qy 601 ACATCAAGTATTTGTTTCTCTGTGAAGAGAACTTAGCTCGGTGTTTAAAGAGCAGAG 660
Db 601 ACATCAAGTATTTGTTTCTCTGTGAAGAGAACTTAGCTCGGTGTTTAAAGAGCAGAG 660
Qy 661 TTAACGC 667
Db 661 TTAACGC 667

RESULT 2

US-10-688-481-6
; Sequence 6, Application US/10688481
; Publication No. US20040194163A1
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSMALDO DA
; APPLICANT: BOHNER, HANS J.
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: 16313-0039
; CURRENT APPLICATION NUMBER: US/10/688,481
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 6
; LENGTH: 667
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-10-688-481-6

Query Match 100.0%; Score 667; DB 8; Length 667;
Best Local Similarity 100.0%; Pred. No. 2.5e-220;
Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCCCGGGTCCGTGATACCAAGCTGTATACATGTTCTTGTAGATTTGTTTACGGCT 60
Db 1 ATCCCGGGTCCGTGATACCAAGCTGTATACATGTTCTTGTAGATTTGTTTACGGCT 60
Qy 61 TTCTTGGAGCATGGGGCTGTGGAGAGAGGCAAAATCTGTTTCTGGGCTTCGACA 120
Db 61 TTCTTGGAGCATGGGGCTGTGGAGAGAGGCAAAATCTGTTTCTGGGCTTCGACA 120
Qy 121 ATGTGCGAAGACTACTTCTTGTGACATGCTCAAGATGAGAACTGGGCGACATCAAC 180
Db 121 ATGTGCGAAGACTACTTCTTGTGACATGCTCAAGATGAGAACTGGGCGACATCAAC 180
Qy 181 CAAGCAGATCAACGTCAGAGAGTTGAGTATCAACAGATGAAGTTCAAGACATTCG 240
Db 181 CAAGCAGATCAACGTCAGAGAGTTGAGTATCAACAGATGAAGTTCAAGACATTCG 240

Db 181 CAAGCAGATCAACGTCAGAGAGTTGAGTATCAACAGATGAAGTTCAAGACATTCG 240
Qy 241 ATCTGGGTGGCCACACATGCTTCGACGCGTGTGGAGGAACTATCTATGTAAAGTGTATG 300
Db 241 ATCTGGGTGGCCACACATGCTTCGACGCGTGTGGAGGAACTATCTATGTAAAGTGTATG 300
Qy 301 CTATAGTATCTCTGTCGACGAGTATGACAGGAGAGATTTGCTGAGTCAAAAGAGAGC 360
Db 301 CTATAGTATCTCTGTCGACGAGTATGACAGGAGAGATTTGCTGAGTCAAAAGAGAGC 360
Qy 361 TCGATTCTCTCTCTCGGAGATTTCTGTGCCAAGTTCTGTGCTGCTGCTGGAAACA 420
Db 361 TCGATTCTCTCTCTCGGAGATTTCTGTGCCAAGTTCTGTGCTGCTGCTGGAAACA 420
Qy 421 AGATTGATATCCCGTACGCTTCTTGAAGAGGTTGGGTTCCACTTGGGTTGACA 480
Db 421 AGATTGATATCCCGTACGCTTCTTGAAGAGGTTGGGTTCCACTTGGGTTGACA 480
Qy 481 TGACCACTGGTAAAGAAAGGAGTGAACCTGGAGATGACCAATTCGGCCCATTTGAGTTT 540
Db 481 TGACCACTGGTAAAGAAAGGAGTGAACCTGGAGATGACCAATTCGGCCCATTTGAGTTT 540
Qy 541 TCATGTGCAATGATTTGTGCGCAAAATGGGGTACGGTGAAGGTTTCAAGTGAATGACCAAGT 600
Db 541 TCATGTGCAATGATTTGTGCGCAAAATGGGGTACGGTGAAGGTTTCAAGTGAATGACCAAGT 600
Qy 601 ACATCAAGTATTTGTTTCTCTGTGAAGAGAACTTAGCTCGGTGTTTAAAGAGCAGAG 660
Db 601 ACATCAAGTATTTGTTTCTCTGTGAAGAGAACTTAGCTCGGTGTTTAAAGAGCAGAG 660
Qy 661 TTAACGC 667
Db 661 TTAACGC 667

RESULT 3

US-09-828-310-1/c
; Sequence 1, Application US/09828310
; Patent No. US20020066124A1
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSMALDO DA
; APPLICANT: BOHNER, HANS J.
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: 16313-0039
; CURRENT APPLICATION NUMBER: US/09/828,310
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 805
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-09-828-310-1

Query Match 98.2%; Score 655; DB 3; Length 805;
Best Local Similarity 100.0%; Pred. No. 4.1e-216;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGGGTCGTGATACCAAGGCTGGTACATGTTCTTGTAGATTTGTTTACGGCTTTCT 64
Db 781 CGGGTCGTGATACCAAGGCTGGTACATGTTCTTGTAGATTTGTTTACGGCTTTCT 722
Qy 65 TGGAGCATGAGGCTGTGGAGAGAGGCAAAATCTGTTTCTGGGCTTCGACAATGC 124
Db 721 TGGAGCATGAGGCTGTGGAGAGAGGCAAAATCTGTTTCTGGGCTTCGACAATGC 662
Qy 125 TGGCAAGACTACTTCTTGTGACATGCTCAAGATGAGAACTGGGCGACATCAAC 184
Db 125 TGGCAAGACTACTTCTTGTGACATGCTCAAGATGAGAACTGGGCGACATCAAC 184

Db 661 TGGCAAGACTACTCTTCTGCAATGCTCAAGATGAGAACTGGGCAACATCAACCAAC 602
QY 185 GCAATATCCAGCGTCAGAGAGTGTATCAACAGAGTGAAGTTCAAGCAATTGCATCT 244
Db 601 GCAATATCCAGCGTCAGAGAGTGTATCAACAGAGTGAAGTTCAAGCAATTGCATCT 542
QY 245 GGGTGGCCACACAAATCGCTCGACCGCTGTGAGGAGCTACTATGTCTAAGTGGATGCTAT 304
Db 541 GGGTGGCCACACAAATCGCTCGACCGCTGTGAGGAGCTACTATGTCTAAGTGGATGCTAT 482
QY 305 AGTATATCTCTGTCGACGCGATGACAGGAGAGATTTGCTGAGTCAAGAAAGAGCTCGA 364
Db 481 AGTATATCTCTGTCGACGCGATGACAGGAGAGATTTGCTGAGTCAAGAAAGAGCTCGA 422
QY 365 TTCTCTTCTCTCCGAGATTCCTGTCCCAAGTTCTGTGCTGTCTGTCTGTGAGAAACAAGAT 424
Db 421 TTCTCTTCTCTCCGAGATTCCTGTCCCAAGTTCTGTGCTGTCTGTCTGTGAGAAACAAGAT 362
QY 425 TGAATATCCGTAACGCTTCTTCTGAAAGACAGATTCGAGTTCAACATTTGGGTTGACATGAC 484
Db 361 TGAATATCCGTAACGCTTCTTCTGAAAGACAGATTCGAGTTCAACATTTGGGTTGACATGAC 302
QY 485 CACTGGTAAAGAACGCGTGAACCTGGAGATGACAACTTCCGCCCATTTGAGGTTTTCAT 544
Db 301 CACTGGTAAAGAACGCGTGAACCTGGAGATGACAACTTCCGCCCATTTGAGGTTTTCAT 242
QY 545 GTGCAATATTTGTCGCGCAAAATGGGGTACGGTGAAGTTTCAAGTGAATGACCAATGACAT 604
Db 241 GTGCAATATTTGTCGCGCAAAATGGGGTACGGTGAAGTTTCAAGTGAATGACCAATGACAT 182
QY 605 CAAGTATGTTTCTTCTGTGAAGAGAACTTAGCTCGGTTGTTAAGAGCGACGA 659
Db 181 CAAGTATGTTTCTTCTGTGAAGAGAACTTAGCTCGGTTGTTAAGAGCGACGA 127

RESULT 4

US-10-688-481-1/c
; Sequence 1, Application US/10688481
; Publication No. US20040194163A1
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSMALDO DA
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, RUYUING
; TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: 16313-0039
; CURRENT APPLICATION NUMBER: US/10/688,481
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 805
; TYPE: DNA
; ORGANISM: Physcomitrella patens
; US-10-688-481-1

Query Match 98.2%; Score 655; DB 8; Length 805;
Best Local Similarity 100.0%; Pred. No. 4,1e-216;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGGGTCCTGATATACCAAGGCTGTACCATGTTCTTTGATGATGGTTTACGGCTTTCT 64
Db 781 CGGGTCCTGATATACCAAGGCTGTACCATGTTCTTTGATGATGGTTTACGGCTTTCT 722
QY 65 TGGGACATATGGGCTGTGGAAGAAGAGGCAAAATCTTCTTGGTCTGACAAATGC 124
Db 721 TGGGACATATGGGCTGTGGAAGAAGAGGCAAAATCTTCTTGGTCTGACAAATGC 662
QY 125 TGGCAAGACTACTCTTCTGCAATGCTCAAGATGAGAACTGGGCAACATCAACCAAC 184

Db 661 TGGCAAGACTACTCTTCTGCAATGCTCAAGATGAGAACTGGGCAACATCAACCAAC 602
QY 185 GCAATATCCAGCGTCAGAGAGTGTATCAACAGAGTGAAGTTCAAGCAATTGCATCT 244
Db 601 GCAATATCCAGCGTCAGAGAGTGTATCAACAGAGTGAAGTTCAAGCAATTGCATCT 542
QY 245 GGGTGGCCACACAAATCGCTCGACCGCTGTGAGGAGCTACTATGTCTAAGTGGATGCTAT 304
Db 541 GGGTGGCCACACAAATCGCTCGACCGCTGTGAGGAGCTACTATGTCTAAGTGGATGCTAT 482
QY 305 AGTATATCTCTGTCGACGCGATGACAGGAGAGATTTGCTGAGTCAAGAAAGAGCTCGA 364
Db 481 AGTATATCTCTGTCGACGCGATGACAGGAGAGATTTGCTGAGTCAAGAAAGAGCTCGA 422
QY 365 TTCTCTTCTCTCCGAGATTCCTGTCCCAAGTTCTGTGCTGTCTGTCTGTGAGAAACAAGAT 424
Db 421 TTCTCTTCTCTCCGAGATTCCTGTCCCAAGTTCTGTGCTGTCTGTCTGTGAGAAACAAGAT 362
QY 425 TGAATATCCGTAACGCTTCTTCTGAAAGACAGATTCGAGTTCAACATTTGGGTTGACATGAC 484
Db 361 TGAATATCCGTAACGCTTCTTCTGAAAGACAGATTCGAGTTCAACATTTGGGTTGACATGAC 302
QY 485 CACTGGTAAAGAACGCGTGAACCTGGAGATGACAACTTCCGCCCATTTGAGGTTTTCAT 544
Db 301 CACTGGTAAAGAACGCGTGAACCTGGAGATGACAACTTCCGCCCATTTGAGGTTTTCAT 242
QY 545 GTGCAATATTTGTCGCGCAAAATGGGGTACGGTGAAGTTTCAAGTGAATGACCAATGACAT 604
Db 241 GTGCAATATTTGTCGCGCAAAATGGGGTACGGTGAAGTTTCAAGTGAATGACCAATGACAT 182
QY 605 CAAGTATGTTTCTTCTGTGAAGAGAACTTAGCTCGGTTGTTAAGAGCGACGA 659
Db 181 CAAGTATGTTTCTTCTGTGAAGAGAACTTAGCTCGGTTGTTAAGAGCGACGA 127

RESULT 5

US-10-767-701-13805
; Sequence 13805, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21 (5353)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 13805
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS2820_1
; US-10-767-701-13805

Query Match 52.4%; Score 349.6; DB 7; Length 954;
Best Local Similarity 76.4%; Pred. No. 5.7e-110;
Matches 443; Conservative 0; Mismatches 134; Indels 3; Gaps 1;

QY 33 ATGTTTCTTGTATGATTTGTTTACGCGCTTCTTGGAGCATAGGCGTGGAGAGAG 92
Db 134 ATGTTTCTTGTATGATTTGTTTACGCGCGTGTGGCGTGCCTTGGGCTGTGGAGAGAG 193
QY 93 GCCAAATCTGTTTCTGGGCTCGACAAATGCTGGCAAGATTAATCTTCTGACATGCTC 152
Db 194 GGAAGATCTTCTTCTGCGCTCGACAAAGCGCGGGAACACACCTCTCCACATGCTC 253
QY 153 AAGATGAGAACTGGGCGCAATCAACCAAGCATATCAAGTCAAGAGAGTGAAT 212
Db 254 AAGACGAGCGGCTGTGACAGACAGCGCATGATCCGACGTCAAGAGAGTGAAT 313


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QY 213 ATCAACGAGTGAAGTTCAAAAGCATTCGATCTGGGTGGCCACACAAATCGCTCGACGGGTG 272
| | | | |
DB 314 ATGGCGAGGATCAAGTTCAAGGGCCCTTGACCTCGGGGGCCACAGATCGCTCGCGGGTTC 373
| | | | |
QY 273 TGGAGGACTACTATGCTAAGAGTGATGATATAGTATCTCGTCGACGAGTAGACAGG 332
| | | | |
DB 374 TGGAGGATTACTACGAAAGGTTGATGCTGTATATCTGGTATGATATGATATGACAG 433
| | | | |
QY 333 GAGAGATTTGCTGAGTCAAAAGAAAGAGCTCGATTCCTTCTCTCCGACGATTCCTGTC 392
| | | | |
DB 434 GAGGATTTGCAAGATCAAAAAGAGCTCGATGCTCTCGTGTGATGATTCCTTGGCC 493
| | | | |
QY 393 CAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 452
| | | | |
DB 494 AATGTTCCATTTTCATCTCTGGCAACAGATTGATATCCATATGCTGCTCTGAAAG 553
| | | | |
QY 453 GAGTTCGCTTCAACATTCGAGTTGACCA--TGACCACTGGTAAAGAAAGGTAAGCTG 509
| | | | |
DB 554 GAGCTACGATATCACTTACGCTTACGACTTCAACACGGGAAGGCAAGTCAACCTT 613
| | | | |
QY 510 GAGAGATGACAACATTCGCGCCCATTTGAGGTTTTCATGTCAGATATTTGCGCAAAATG 569
| | | | |
DB 614 GGTGATCCCAATGTCGCGCCCATTTGAGGTTTTCATGTCAGATATTTGTCGAAGATG 673
| | | | |
QY 570 TACGTTGAAGTTTCAAGTGTGATGATGCCAGTACATCAAGT 609
| | | | |
DB 674 TACGTTGATGTTTCAAGTGTGATGATGCCAGTACATCAAGT 713
| | | | |
```

RESULT 6

```
US-10-425-114-7242
; Sequence 7242, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 7242
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700623579_F1
US-10-425-114-7242
```

Query Match 51.0%; Score 340.4; DB 7; Length 998;
Best Local Similarity 74.7%; Pred. No. 9.1e-107;
Matches 441; Conservative 0; Mismatches 146; Indels 3; Gaps 1;

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QY 23 GGCTGTACCAATGTTCTGTGATGTTTACGGCTTCTGCGAGCATAGGGCTGTG 82
| | | | |
DB 156 GGTGGGGAGATGTTCTCTGGAGCTGATCTACGGGGTGTGGCTCTCCCTCGGCTGTG 215
| | | | |
QY 83 GCAGAAAGAGGCAAAATCTGTTTCTGGGTCTGACAAATCTGCAAGACTACTCTTCT 142
| | | | |
DB 216 GCAAGAGAGGCAAAATCTCTTCTGCTCGACAAAGCGGGAAGACAGCTGCT 275
| | | | |
QY 143 GCACATGCTCAAGATGAGAACTGGGGCAACATCAACCAAGCATATTCACATGTCAGA 202
| | | | |
DB 276 CCACATGCTCAAGAGACGAGCGGTTGTGACACACAGCCGACGACGACGACGTCGGA 335
| | | | |
QY 203 GGAATGATATCAACAGAGTGAAGTTCAAGCATTTGATCTGGGTGGCCACAAATCGC 262
| | | | |
DB 336 GGAAGCTCAGCATCGCAAGATCAAGTTCAAGCGTTTCAAGCTCGGCGCCACAGATCGC 395
| | | | |
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QY 263 TCGACCCGTTGGAGGAGACTATATCTAAGTGAATGCTATATGTTATCTGTCAGCG 322
| | | | |
DB 396 GCGCCCGCTGTGGAGAGATTACTACCAAGAGTTGATGCTGATGATATCTGTTAGATGC 455
| | | | |
QY 323 AGTAGACAGGAGAGATTTGCTGAGTCAAGAAAGAGCTGATTTCTTCTCTCCGACGA 382
| | | | |
DB 456 ATATGATTAAGAGCCGATTTGCTGATCAATCAAGAAAGAGCTGATGCTCTCTGTTATGA 515
| | | | |
QY 383 TTCTGTGCTCAAGTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 442
| | | | |
DB 516 TTCTTTGGCAATGTTCCATTTCTCATCTTGTGCAACAGATGATATCCATATGCTGCG 575
| | | | |
QY 443 TTCTGAAGACAGATTGCGGTTACACTTGGGTGACCA--TGACCACTGTTAAAGAAC 499
| | | | |
DB 576 CTCTGAAGAGAGCTACCGGATCACTAGCCCTTACCACTTCAACACGGGAAGGCA 635
| | | | |
QY 500 GGTGAACCTGGGAGATAGCAACATTCGCGCCATTTGAGTTTTCATGTCAGTATGTCG 559
| | | | |
DB 636 GGTCAACCTTTGGGACTCCCATATGTCCTGCTGCTGAGTCTTCAATGTCAGTGTGTCG 685
| | | | |
QY 560 CAAATGCGGTACGATGAGTTTCAAGTGTGATGATGCCAGTACATCAAGT 609
| | | | |
DB 696 CAGATGGGCTACGATGATGTTTCAAGTGGTCTCCAGTATCAAGT 745
| | | | |
```

RESULT 7

```
US-10-425-115-14342
; Sequence 14342, Application US/10425115
; Publication No. US200400214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 14342
; LENGTH: 1221
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_62205C.1
US-10-425-115-14342
```

Query Match 51.0%; Score 340.4; DB 8; Length 1221;
Best Local Similarity 74.7%; Pred. No. 1e-106;
Matches 441; Conservative 0; Mismatches 146; Indels 3; Gaps 1;

```
QY 23 GGCTGTACCAATGTTCTGTGATGTTTACGGCTTCTTGGCAAGCATAGGGCTGTG 82
| | | | |
DB 229 GGTGGGGAGATGTTCTCTGGAGCTGTTCTACGGGGTGTGGCTCTCCCTCGGCTGTG 288
| | | | |
QY 83 GCAGAAAGAGGCAAAATCTGTTTCTGGGTCTGCAAAATCTGCAAGACTACTCTTCT 142
| | | | |
DB 289 GCAAGAGAGGCAAAATCTCTTCTGCTCGACAAAGCGGGAAGACAGCTGCT 348
| | | | |
QY 143 GCACATGCTCAAGATGAGAACTGGGGCAACATCAACCAAGCATATTCACATGTCAGA 202
| | | | |
DB 349 CCACATGCTCAAGAGACGAGCGGTTGTGACACACAGCCGACGACGACGTCGGA 408
| | | | |
QY 203 GGAATGATATCAACAGAGTGAAGTTCAAGCATTTGATCTGGGTGGCCACAAATCGC 262
| | | | |
DB 409 GGTGCTCAGATGCGCAAGATTAAGTTCAAGGTTTGAACCTTGGCGGCTCACAGATGCG 468
| | | | |
QY 263 TCGACGCGTGGAGGAGACTATATGCTAAGTGTGATGATGATATCTGTCAGCGC 322
| | | | |
DB 469 GCGCCGCTGTGAGAGATTAACGCAAGGTTGATGCTGTATATCTGTTAGATGC 528
| | | | |
```


Qy	323	IGTGAAGAGGAGAGATTTTGTCTGATGCTCAAGAAAGAGCTGATTTCTTCTCTGCGACGA	382
Db	529	ATATGATTAAGAGGCAATTTGTCTGAATCAAAAGAGAGCTGAGAGCTCTCTGTCTGATGA	588
Qy	383	TTCTCTGTCCCAAGTTTCTGTGCTGTGCTCTGTGGGAAAACAAGATTGATATCCGTACGCTTC	442
Db	589	TTCTTTGGCCAAATGTTTCCATTTTCTCATCTTTGGCAACAAAGATTGATATGCCATATGCTGC	648
Qy	443	TTCTGAAGACGAGTTTCCGTTTCAACTTTGGGTTGACCA--TGACCATGTGTAAAGAAAC	499
Db	649	CTCTGAAGAGGAGCTACCGGTATCATCCTAGGCGCTTGGCACTTACACAAACGGGAAAGGSCAA	708
Qy	500	GGTGAACCTTGGAGATATGAAACATTCGCGCCATTGAGGTTTTCATATGTGACGATATTTGGCG	559
Db	709	GGTCAACCTTTGGCGAGCTCCAAATGTCGCTCACCTTGAGGCTTTCATATGTGACGATGTTGTCG	768
Qy	560	CAAAATGGGGGTACGGGTGAAGTTTCAAGTGAATGACCCAGTACATCAAGT	609
Db	769	CAAGATGGGCTACGGGTGATGTTTCAAGTGGGCTCTCCAGTACATCAAGT	818
RESULT 8			
US-10-425-115-143343			
: Sequence 143343, Application US/10425115			
: Publication No. US20040214272A1			
: GENERAL INFORMATION:			
: APPLICANT: La Rosa, Thomas J.			
: APPLICANT: Kovalic, David K.			
: APPLICANT: Zhou, Yihua			
: APPLICANT: Cao, Yongwei			
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With			
: TITLE OF INVENTION: Plants			
: FILE REFERENCE: 38-21(5322)B			
: CURRENT APPLICATION NUMBER: US/10/425,115			
: CURRENT FILING DATE: 2003-04-28			
: NUMBER OF SEQ ID NOS: 369326			
: SEQ ID NO 143343			
: LENGTH: 1645			
: TYPE: DNA			
: ORGANISM: Zea mays			
: FEATURE:			
: OTHER INFORMATION: Clone ID: MRT4577_62206C.1			
US-10-425-115-143343			
Query Match			
Best Local Similarity 74.7%; Score 340.4; DB 8; Length 1645;			
Matches 441; Conservative 0; Mismatches 146; Indels 3; Gaps 1;			
Qy	23	GGCTGTACATGTTTCTTGTAGATTGTTTACGGCTTCTTTCGACGATAGGGCTGTG	82
Db	336	GGTGGGGAGATGTTCTCTGTGGACGTGTTACGGGGGTGGCTGCCCTCGGGCTGTG	395
Qy	83	GCAGAAAGGAGCCAAATCTGTTTCTGGGTCTCGACATGCTGGGAAGACTACTCTTCT	142
Db	396	GCAGAAAGGAGCCAAAGATCTCTTCTTGGCTCTGCAACGCGGGCAAGACAGCTGCT	455
Qy	143	GCACATGTCTCAAGATGAGAAACTGGGGCAACATCAACAAACGACATATCAACGTGAG	202
Db	456	CCACATGTCTCAAGAGAGAGCGGTGTGTGACAGACACAGCGAGCAGACACCCAGAGCTCGA	515
Qy	203	GGAGTTGACTATCAACAGAGTGAAGTTTCAAAGCATTTGATCTGGGTGGCCACAAATGCG	262
Db	516	GGAGTCTAGCATCTGGAGATCAAGTTTCAAAGGCTTTCGACTTCGGGGGCCACCAAGATGCG	575
Qy	263	TGAGAGCGGTGTGAGGAGACTATGATAGTGAAGTGAATGATATGATGTCGACGC	322
Db	576	GCGCCGCGTGTGAGAGATTTACTACGCAAAAGTTGATGCTGATATCCTGGTAGTGC	635
Qy	323	ACTAGACAGGAGAGATTTTGTCTGAGTCAAAAGAAAGACTGATTTCTTCTTCCGACGA	382
Db	636	ATATGATTAAGAGGCAATTTGTCTGAATCAAAAGAGAGGCTGAGTCTCTGTCTGATGA	695
Qy	383	TTCTCTGTCCCAAGTTTCTGTGCTGTGCTCTGTGGGAAAACAAGATTGATATCCGTACGCTTC	442

[illegible]

Db 589 CGGCTTGAAGAGAGAGCTGGCTACTACCTTGGCTGAGCACTTCAACGGGGAAG 648
Qy 496 GAACGGTGAACCTGGAGATAGCAACATTCGCCCATTTGAGTTTTCATGTGAGTATTTG 555
Db 649 GCAACGTGAACCTTGGCTGATTCGAATGTGGCCCCCTGGAGATCTTCATGTGAGTGTGG 708
Qy 556 TGGCGCAAAATGGGGTATGCGTGAAGTTTCAAGTGGATGACCCAGTACATCAAGTGA 611
Db 709 TGGCGCAAGATGGGCTATGTGGAAGGCTTCAATGATGTCTCATGATCATCAAGTGA 764

RESULT 10

US-10-425-114-21639
; Sequence 21639, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 21639
; LENGTH: 955
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3354-056-D12_FLI
US-10-425-114-21639

Query Match 50.3%; Score 335.6; DB 7; Length 955;

Best Local Similarity 73.7%; Pred. No. 4,1e-105;

Matches 441; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

Qy 19 CCAAGGCTGTACATGTTCTTGTAGATTGTTTACCGCTTCTTGCAGATAGGGC 78
Db 84 CCGAGTTGTAAAGATGTTCTGTGAGCTGTGTTCTATGGGCTGTGATCGTTGGGC 143
Qy 79 TGTGCGAAGAGAGAGCCAAATCTGTTTCTGGGCTTCGACATGTGCGAAGTATCTC 138
Db 144 TGTGCGAAGAGAGAGCTTAAGATCTCTTCTTGGCTTCGACAGCGCGGCAAGCACCC 203
Qy 139 TTCTGCACATGCTCAAGATAGAAACTGGGGCAACATCAACGCGATATCAAGCT 198
Db 204 TCTTCCACATGCTCAAGAGCAGCGGCTCTGACAGCACAGCCAAAGCAGTACCCACGT 263
Qy 199 CAGAGAGTTGAGTATCAACAGAGTGAAGTTCAAGAGATTCGATCTGGTGGCCACAA 258
Db 264 CAGAGAGTTGAGTATGCGAGATCGGACATCAAGTTCAAGGCTTGAAGCTTGGGGCCACAGA 323
Qy 259 TCGCTGACGCGGTGAGAGGACTACTATGCTAAAGTGAATGCTATAGTATCTCGTCG 318
Db 324 TCGCGCGCGGCTCGAAGAGACTATACGCAAGTTGATGCTGTGTGTAATCTTGGTGG 383
Qy 319 ACCGAGTGAACAGGAGAGATTTGCTGAGTCAAAAGAAAGACTGATTTCTTCTTCG 378
Db 384 ATGCTGTGACAAAGAGAGTTTGGCCGAGTGAAGAAAGAGCTGATCGCTTCTTCAG 443
Qy 379 ACGATTTCTGTCCCAAGTTCTGTGCTGCTCGTGGGAAACAAGATTGATATCCCGTACG 438
Db 444 ATGACTCCCTTGCAGAACTCTTCTTCATATCTGGGCAACAAGATTGACATCCCATACG 503
Qy 439 CTTCCTTGAAGACGAGTTGCGTTTCACTTGGGTTGACCA--TGACCACTGGTAAAG 495
Db 504 CGGCTTCAAGAGAGAGCTGAGTACTACTCTCGGCTGAGCAATTCACAAACGGGAAG 563
Qy 496 GAACGGTGAACCTGGAGATAGCAACATTCGCGCCCATTTGAGTTTCAATGTGAGTATTTG 555

Db 564 GCAACGTGAACCTTGGCGGACTCCCAACGTCGCCCTCGAGATCTTCAATGTGAGTGTGG 623
Qy 556 TGGCGCAAAATGGGGTATGCGTGAAGTTTCAAGTGAAGTACCCAGTACATCAAGTATTTG 613
Db 624 TGGCGCAAGATGGGCTATGTGGAAGGCTTCAATGATGTCTCATGATCATCAAGTGTGG 681

RESULT 11

US-10-425-114-13536
; Sequence 13536, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 13536
; LENGTH: 966
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB143-001-F4_FLI
US-10-425-114-13536

Query Match 49.8%; Score 332.4; DB 7; Length 966;

Best Local Similarity 73.4%; Pred. No. 5,4e-104;

Matches 439; Conservative 0; Mismatches 156; Indels 3; Gaps 1;

Qy 19 CCAAGGCTGTACATGTTCTTGTAGATTGTTTACCGCTTCTTGCAGATAGGGC 78
Db 116 CCGAGTTGTAAAGATGTTCTGTGAGCTGTGTTCTATGGGCTGTGATCGCTTGGGC 175
Qy 79 TGTGCGAAGAGAGAGCCAAATCTGTTTCTGGGCTTCGACATGTGCGAAGTATCTC 138
Db 176 TGTGCGAAGAGAGAGCTTAAGATCTCTTCTTGGCTTCGACAGCGCGGCAAGCACCC 225
Qy 139 TTCTGCACATGCTCAAGATAGAAACTGGGGCAACATCAACGCGATATCAAGCT 198
Db 236 TCTTCCACATGCTCAAGAGCAGAGCGGCTCTGACAGCACAGCCAGCAGTACCCACGT 255
Qy 199 CAGAGAGTTGAGTATCAACAGAGTGAAGTTCAAGAGATTCGATCTGGTGGCCACAA 258
Db 296 CAGAGAGTTGAGTATGCGAGATCGGACATCAAGTTCAAGGCTTGAAGCTTGGGGCCACAGA 355
Qy 259 TCGCTGACGCGGTGAGAGGACTACTATGCTAAAGTGAATGCTATAGTATCTCGTCG 318
Db 356 TCGCGCGCGGCTCGAAGAGCTACTACGCCAAGGTGATGTGTGTACTTGGTGG 415
Qy 319 ACCGAGTGAACAGGAGAGATTTGCTGAGTCAAAAGAAAGACTGATTTCTTCTTCG 378
Db 416 ATGCTGTGACAAAGAGAGCTTTGGCGAGTCAAGAAAGAGCTTGAATGCCCTTTCAG 475
Qy 379 ACGATTTCTGTCCCAAGTTCTGTGCTGCTCTTGGGAAAACAAGATTGATATCCCGTACG 438
Db 476 ATGACTCCCTTGCAGAACTCTTCTTCATATCTGGGCAACAAGATTGACATCCCATACG 535
Qy 439 CTTCCTTGAAGACGAGTTGCGTTTCACTTGGGTTGACCA--TGACCACTGGTAAAG 495
Db 536 CGGCTTCAAGAGAGAGCTGAGTACTACTCTCGGCTGAGCAATTCACAAACGGGAAG 595
Qy 496 GAACGGTGAACCTGGAGATAGCAACATTCGCGCCCATTTGAGTTTCAATGTGAGTATTTG 555
Db 596 GCAACGTGAACCTTGGCGGACTCCCAATGTCCGGCCCTTGGAGATCTTCAATGTGAGTGTGG 655

Qy 556 TGGCAAAATGGGGTACGGTGAAGTTTTCAGTGTGATGACCCAGTACATCAATGATGATT 613
Db 656 TGGCAAAATGGGGTATGGGGAAGGCTTCAATGATGTCTGATCATCAATGATGAGT 713

RESULT 12
US-10-425-114-33380
; Sequence 33380, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 33380
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17103E09_FLI
US-10-425-114-33380

Query Match 49.8%; Score 332.4; DB 7; Length 1017;
Best Local Similarity 73.4%; Pred. No. 5,5e-104;

Matches 439; Conservative 0; Mismatches 156; Indels 3; Gaps 1;

Qy 19 CCAAGGCTGTACATGTTCTTGTAGATTGTTTACCGCTTCTTGCAGATAGGCG 78
Db 97 CCGAGTTTAAAGATGTTCTGTGTGACTGTTCTATGGGGTGTGGCATCGCTTGGGC 156
Qy 79 TGTGGCAAGAGAGGCCAAATCTCTGTTTGTGGGTCTTGCATGCTGGCAAGATCTATC 138
Db 157 TGTGGCAAGAGAGGCTTAAATCTCTTCTTGGCCCTGCAACGCGGCAAGACCAACC 216
Qy 139 TTCTGCATGCTCAAGATGAGAACTGGGGCAATCAACCAAGCATATCAACGT 198
Db 217 TCTTCAATGCTGAAAGAGAGCGGCTCTTACGACCAAGCCGACATCAACGT 276
Qy 199 CAGAGAGTTGATATCAACAGATGAAGTTCAAGCATTCGATCTGGGTGGCACA 258
Db 277 CAAAGAGTTGAGATCGGAGATCAAGTTCAAGGCTTCGACTTGGGGGCAACAGA 336
Qy 259 TCGCTGACGCGTGTGGAGGACTATGCTAAAGTGTGATGCTATAGTATCTGCTG 318
Db 337 TCGCCGCGCGCTGTGGAGACTACACCAAGGTTGATGCTGTGTACTTGGTGG 396
Qy 319 AGCAGTAGACAGAGGAGATTGCTGAGTCAAGAAAGAGCTCGATCTCTCTCCG 378
Db 397 ATCTGTGACAAAGAACTTTGCGAGTCAAGAAAGAGCTTGAAGCTCTTCTTGAC 456
Qy 379 ACGATTCTGTGCTCCAGTCTGTGCTGCTCTCTGGGAAACAAGATTGATCCGTA 438
Db 457 ATGACTCCTTGGAAAGCTTCTTCTCTCATCTGGGCAACAAGATTGATCCCAACG 516
Qy 439 CTTCTTCTGAAGACGAGTTGCGGTTCACTTGGGTGACCA--TGACCACTGGTAAG 495
Db 517 CCGCTTCAAGAGAGAGCTGAGTACTACCTCGGCTGAGCAACTTCACAAACGGGAAG 576
Qy 496 GAACGCTGAACCTGGAGATAGCAACATGGGCCCATTTGAGGTTTTCATGAGCAT 555
Db 577 GCAACGTGAACCTGGCGACTCCATGTCGCGCCCTGAGAGATCTTATGAGCATG 636
Qy 556 TGGCAAAATGGGGTACGGTGAAGTTTTCAGTGTGATGACCCAGTACATCAATGAT 613
Db 637 TGGCAAAATGGGGTATGGGGAAGGCTTCAATGATGTCTGATCATCAATGATGAGT 694

RESULT 13
US-10-425-115-98354

; Sequence 98354, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 98354
; LENGTH: 1334
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: MRT4577_21209C.1
US-10-425-115-98354

Query Match 49.8%; Score 332.4; DB 8; Length 1334;
Best Local Similarity 73.4%; Pred. No. 6,4e-104;

Matches 439; Conservative 0; Mismatches 156; Indels 3; Gaps 1;

Qy 19 CCAAGGCTGTACATGTTCTTGTAGATTGTTTACCGCTTCTTGCAGATAGGCG 78
Db 257 CCGAGTTTAAAGATGTTCTGTGTGACTGTTCTATGGGGTGTGGCATCGCTTGGGC 316
Qy 79 TGTGGCAAGAGAGGCCAAATCTCTGTTTGTGGGTCTTGCATGCTGGCAAGATCTATC 138
Db 317 TGTGGCAAGAGAGGCTTAAATCTCTTCTTGGCCCTGCAACGCGGCAAGACCAACC 376
Qy 139 TTCTGCATGCTCAAGATGAGAACTGGGGCAATCAACCAAGCATATCAACGT 198
Db 377 TCTTCAATGCTGAAAGAGAGCGGCTCTTACGACCAAGCCGACATCAACGT 436
Qy 199 CAGAGAGTTGATATCAACAGATGAAGTTCAAGCATTCGATCTGGGTGGCACA 258
Db 437 CAAAGAGTTGAGATCGGAGATCAAGTTCAAGGCTTCGACTTGGGGGCAACAGA 496
Qy 259 TCGCTGACGCGTGTGGAGGACTATGCTAAAGTGTGATGCTATAGTATCTGCTG 318
Db 497 TCGCCGCGCGCTGTGGAGACTACACCAAGGTTGATGCTGTGTACTTGGTGG 556
Qy 319 AGCAGTAGACAGAGGAGATTGCTGAGTCAAGAAAGAGCTCGATCTCTCTCCG 378
Db 557 ATCTGTGACAAAGAACTTTGCGAGTCAAGAAAGAGCTTGAAGCTCTTCTTGAC 616
Qy 379 ACGATTCTGTGCTCCAGTCTGTGCTGCTCTCTGGGAAACAAGATTGATCCGTA 438
Db 617 ATGACTCCTTGGAAAGCTTCTTCTCTCATCTGGGCAACAAGATTGATCCCAACG 676
Qy 439 CTTCTTCTGAAGACGAGTTGCGGTTCACTTGGGTGACCA--TGACCACTGGTAAG 495
Db 677 CCGCTTCAAGAGAGAGCTGAGTACTACCTCGGCTGAGCAACTTCACAAACGGGAAG 736
Qy 496 GAACGCTGAACCTGGAGATAGCAACATGGGCCCATTTGAGGTTTTCATGAGCAT 555
Db 737 GCAACGTGAACCTGGCGACTCCATGTCGCGCCCTGAGAGATCTTATGAGCATG 796
Qy 556 TGGCAAAATGGGGTACGGTGAAGTTTTCAGTGTGATGACCCAGTACATCAATGAT 613
Db 797 TGGCAAAATGGGGTATGGGGAAGGCTTCAATGATGTCTGATCATCAATGATGAGT 854

RESULT 14
US-10-425-114-20345
; Sequence 20345, Application US/10425114


```
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 20345
LENGTH: 986
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3180-039-D5_FLI
US-10-425-114-20345
```

```
Query Match 49.5%; Score 330.4; DB 7; Length 986;
Best Local Similarity 74.3%; Pred. No. 2.7e-103;
Matches 431; Conservative 0; Mismatches 146; Indels 3; Gaps 1;
```

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QY 33 ATGTTCTTGATGATGTTTACGGCTTTCTTGCAGCATAGGGCTGTGGCAGAGAG 92
DB 130 ATGTTCTTGATGATGTTTACGGCTTTCTTGCAGCATAGGGCTGTGGCAGAGAG 189
QY 93 GCCAAATCTGTTCTGAGGCTCTGACAAATGCTGCAAGACTCTTCTGACATGCTC 152
DB 190 GCGAAGATCTCTCTCTGAGGCTCTGACAAATGCTGCAAGACTCTTCTGACATGCTC 249
QY 153 AAGATGAGAACTGAGGCAATCAACCAAGCATATCCAGTCAAGAGAGTTAGT 212
DB 250 AAGACGAGCGGTTGTCAGACACCGCAGCAGCAGCAGTGGAGAGACTCAAGC 309
QY 213 ATCAACAGATGAGTTCAAGACTTGCATCTGGGTGGCCACACATCTGCTGACAGCTG 272
DB 310 ATCGGCAAGATCAAGTTCAAGCTTGCACCTCGCGGCCACAGATCGCGCGCGCTC 369
QY 273 TGAAGGACTACTATGCTAAGGTGATCTATGATCTCTGCTGACAGCATGACAG 332
DB 370 TGAAGGACTACTATGCTAAGGTGATCTATGATCTCTGCTGACAGCATGACAG 429
QY 333 GAGGATTTGCTGATGCAAAAGAGCTGATCTCTCTCTGCTGACAGCATGACAG 392
DB 430 GAGGATTTGCTGATGCAAAAGAGCTGATCTCTCTCTGCTGACAGCATGACAG 489
QY 393 CAAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 452
DB 490 AATGTTCCATTTCTCATCTTCTGCAACAAAGATGATCTCTGCTGCTGCTGCTGCA 549
QY 453 GAGTTGCGTTCACTTGGGTTGACCA--TGACCACTGTTAAAGAACGTTGACCTG 509
DB 550 GAGTGGCGGTATCACTGAGCCTTAGCACTTCAACCGGGAAGGCAAGTCAACTT 609
QY 510 GGAATGACCAATTCGCGCCATTTGAGGTTTTCATGTCATATTTGCGCAAAATGGG 569
DB 610 GCGCATCTCAATGTCGCGCCACTTGAAGGTTTTCATGTCATATTTGCGCAAAATGGG 669
QY 570 TACGGTGAAGTTTCAAGTGAATGACCCAGTACATCAAGT 609
DB 670 TACGGTGAAGTTTCAAGTGAATGACCCAGTACATCAAGT 709
```

```
RESULT 15
US-10-425-114-20291
Sequence 20291, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
```

```
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 20291
LENGTH: 1051
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3180-021-F8_FLI
US-10-425-114-20291
```

```
Query Match 49.5%; Score 330.4; DB 7; Length 1051;
Best Local Similarity 74.3%; Pred. No. 2.8e-103;
Matches 431; Conservative 0; Mismatches 146; Indels 3; Gaps 1;
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```
QY 33 ATGTTCTTGATGATGTTTACGGCTTTCTTGCAGCATAGGGCTGTGGCAGAGAG 92
DB 155 ATGTTCTTGATGATGTTTACGGCTTTCTTGCAGCATAGGGCTGTGGCAGAGAG 214
QY 93 GCCAAATCTGTTCTGAGGCTCTGACAAATGCTGCAAGACTCTTCTGACATGCTC 152
DB 215 GCGAAGATCTCTCTCTGAGGCTCTGACAAATGCTGCAAGACTCTTCTGACATGCTC 274
QY 153 AAGATGAGAACTGAGGCAATCAACCAAGCATATCCAGTCAAGAGAGTTAGT 212
DB 275 AAGACGAGCGGTTGTCAGACACCGCAGCAGCAGCAGTGGAGAGACTCAAGC 334
QY 213 ATCAACAGATGAGTTCAAGACTTGCATCTGGGTGGCCACACATCTGCTGACAGCTG 272
DB 335 ATCGGCAAGATCAAGTTCAAGCTTGCACCTCGCGGCCACAGATCGCGCGCGCTC 394
QY 273 TGAAGGACTACTATGCTAAGGTGATCTATGATCTCTGCTGACAGCATGACAG 332
DB 395 TGAAGGACTACTATGCTAAGGTGATCTATGATCTCTGCTGACAGCATGACAG 454
QY 333 GAGGATTTGCTGATGCAAAAGAGCTGATCTCTCTCTGCTGACAGCATGACAG 392
DB 455 GAGGATTTGCTGATGCAAAAGAGCTGATCTCTCTCTGCTGACAGCATGACAG 514
QY 393 CAAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 452
DB 515 AATGTTCCATTTCTCATCTTCTGCAACAAAGATGATCTCTGCTGCTGCTGCA 574
QY 453 GAGTTGCGTTCACTTGGGTTGACCA--TGACCACTGTTAAAGAACGTTGACCTG 509
DB 575 GAGTGGCGGTATCACTGAGCCTTAGCACTTCAACCGGGAAGGCAAGTCAACTT 634
QY 510 GGAATGACCAATTCGCGCCATTTGAGGTTTTCATGTCATATTTGCGCAAAATGGG 569
DB 635 GCGCATCTCAATGTCGCGCCACTTGAAGGTTTTCATGTCATATTTGCGCAAAATGGG 694
QY 570 TACGGTGAAGTTTCAAGTGAATGACCCAGTACATCAAGT 609
DB 695 TACGGTGAAGTTTCAAGTGAATGACCCAGTACATCAAGT 734
```

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Search completed: December 9, 2005, 01:28:19
Job time : 800 secs
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DY 388 TGTCCCAAGTTCCTGCTGCTCCTCGGAAAACAAGTTGAATACCGTAGCTTCTTG 447
| | | | | | | | | | | | | | | | | | | | | |
Db 505 TAAGTTGTGTGCCAAGTGCATCTTTGGTAATAAGCAGAAATTGCTCACAGAGCCCTG 564

```

RESULT 2
US-10-750-185-27986/c
? Sequence 27986, Application US/10750185
? Publication No. US20050260603A1
? GENERAL INFORMATION:
? APPLICANT: MMI GENOMICS, INC.
? APPLICANT: DENISE, Sue K.
? APPLICANT: KERR, Richard
? APPLICANT: ROSENFELD, David
? APPLICANT: HOLM, Tom
? APPLICANT: BATES, Stephen
? APPLICANT: FANTIN, Dennis
? TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
? FILE REFERENCE: MM1100-2
? CURRENT APPLICATION NUMBER: US/10/750,185
? CURRENT FILING DATE: 2003-12-31
? PRIOR APPLICATION NUMBER: US 60/437,482
? PRIOR FILING DATE: 2002-12-31
? NUMBER OF SEQ ID NOS: 64922
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 27986
? LENGTH: 2946
? TYPE: DNA
? ORGANISM: Bovine 19866880857076
US-10-750-185-27986

```

Query Match	10.3%	Score 68.8	DB 6	Length 2946
Best Local Similarity	69.1%	Pred. No. 8.1e-14		
Matches	94	Conservative	0	Mismatches 42
				Indels 0
				Gaps 0
QY	60	TTTCTTGAGCATATGAGCTGTGGCAGAAAGGCCAAATCTCTTTCTTGSGTCTGCAC	119	
DB	159	TTATTTTCTTTTATAGACTCTACAGAAATGTGAAAACTGTATTTCTTGGGTTTGGAC	100	
QY	120	AATGCTGCAGAACTACTCTTTCTGCACATGCTCAAGATGAGAAACTGGGCGACATCAA	179	
DB	99	AATGAGGCGAAAACCACTCTTCTACACATGCTCAAGAATGACAGACTGGGCGCATGTT	40	
QY	180	CCAAAGCAGTATCCAA	195	
DB	39	CCAAAGTTACATCCAA	24	

```

RESULT 3
US-10-821-234-226
; Sequence 226, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PL_SEQ_gene Version 1.0
; SEQ ID NO 226
; LENGTH: 2960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-226

```

Query Match	8.6%;	Score 57.2;	DB 6;	Length 2960;
Best Local Similarity	48.7%;	Pred. No. 1e-09;		

	Matches	186;	Conservative	0;	Mismatches	193;	Indels	3;	Gaps	1;
Oy	79	TGTGGCAAGAGAGCCAAAATCCTGTTTCTGGGTTCGACAATGCTGGCAAGACTACTC	138							
Db	221	TCTGAAAGGAAGAGATGAGCTGACGCTCGTGGGCTGCACTACTCGGGCAAGACCACT	280							
Oy	139	TTTCGCACATGCTCAAGGATGAGAAACTGGGGCAACAT---CAACCAACGACGATGCCAA	195							
Db	281	TCTGCATGTTCATCGCCTCAGGTCAATTCACTGAAGATATATATCCCAAGTGGCTTCA	340							
Oy	196	CGTCAGAGAGATTAGTATCAACAGAGTGAAGTTCAAAGCATTTGATTTGGGTGGCCACA	255							
Db	341	ACATGAGGAAGGTAACTTAAGTTAACTCAAAATAAAGATCTGGGACATAGAGAGCAAC	400							
Oy	256	CAATCGCTCCAGCGGTGTGAGAGGAGACTATATGCTTAAGTGGATGCTATAGTATCTCG	315							
Db	401	CCCGATTTCCGAAGCATGTGGAGGCGGTATTCAGAGAGATCAATAGTCTATGTTTACATGA	460							
Oy	316	TCGACGCAGTGAGACAGAGAGAGATTTGCTGAGTCAAAAGAAAGAGCTCATTTCTTCT	375							
Db	461	TAGATGTGCGAGATCTGTGAATAAAGATGAAGCTTCCGAAATGAGGTACATATCTTTAG	520							
Oy	376	CCGACGATTTCTGTCCCAAGTTTCTGTGCTGTCTCTGGAAAACAAATTGATATCCGCT	435							
Db	521	ATTAACCAACAGTTTCAAGGAATTCAGGTCTATGCTTGGAAAACAAAGAGATCTTCTTA	580							
Oy	436	ACGCTTCTTTGAAAGACGATT	457							
Db	581	ATGCTTGATGAGAAACGCT	602							

```

RESULT 4
US-10-750-185-37034/C
; Sequence 37034, Application US/10750185
; Publication No. US2005026063A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37034
; LENGTH: 824
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-37034 1986680402345

```

Query Match	Similarity	8.5%	Score 56.6	DB 6	Length 824
Beet Local	Similarity 52.3%		Pred. No. 8e-10		
Match 125	Conservative	0	Mismatches 11	Indels	Gaps 0
QY	216	AACAGAGTGAAGTTCAAAGCATTCGATCTGGGTGGCCACACATGCTCGACGCGGTGG	275		
DB	792	AAAGGTGCTGGCTCAGCTCAGGTCGGGACGTTGGAGGACAAAGAAATAGAGCCACGTTGG	733		
QY	216	AGGAGCTACTATGCTAAGGTGATGCTCTTAAGTGTATCTCGTCGACGCACTAACAAGGAG	335		
DB	732	GGCCCTCACTGTGAGAACACATGATGGGCTAGTGTATGTTGGACACATACACACACAG	673		
QY	336	AGATTGTGAGTCAAAAGAAAGTCGATCTCTTCTCTCGACGATCTCTGTCCCAA	395		
DB	672	CGACTTGAAGACTCCAGAAAGAGTTTATGACACATCTTGAAGATGATGACTTAAATAT	613		

Qy 396 GTTCTGTGCTCTCTGCGGAAACAAGATTATCCGCTTCTTCTGAGACGA 454
Db 612 GTCCCTGTGTCTCTGTTAGCCAAACAAGATTATGCTGAGACTTAAGTCCGACGA 554

RESULT 5
US-10-821-234-76/c
; Sequence 76, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Seache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methode for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 76
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-76

Query Match 7.3%; Score 48.8; DB 6; Length 1650;
Best Local Similarity 46.1%; Pred. No. 6.9e-07;
Matches 164; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

Qy 85 AGAAGAGGCAAAATCTCTGTTCTGCTGCTGCAATGCTGGCAGACTACTCTTCG 144
Db 1359 AGAAGAGATGCCCATTTTATGATGATGATGATGATGATGATGATGATGATG 1300
Qy 145 ACATGCTCAGATGAGAGAACTGGGGCAATCAACCAACGAGTATCCAACTCAGAG 204
Db 1299 ATTAAGTGAAGTTAGGGGAGATGATGATGATGATGATGATGATGATGATG 1240
Qy 205 AGTTGATATCAACAGATGAGATGATGATGATGATGATGATGATGATGATG 264
Db 1239 CAGTGAATATTAAGAACATTTGTTTCAAGATGAGATGATGATGATGATG 1180
Qy 265 GAGCGGTGAGAGGACTACTATGATGATGATGATGATGATGATGATGATG 324
Db 1179 GGCCTCTGTGAGAGATTTACTTCCAGAAATCCAGAGGCTTATTTTGTGTAGATGCA 1120
Qy 325 TAGACAGGAGAGATTTGCTGAGTCAAGAAAGAGCTCGATTTCTCTCCGAGAT 384
Db 1119 ACATGCTGTAAGAAATTCAGAGATGAGATGAGATGAGATGAGATGAGATG 1060
Qy 385 CTCGTGCCAAGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 440
Db 1059 AATTGAGATGACAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1004

RESULT 6
US-11-093-746A-15
; Sequence 15, Application US/11093746A
; Publication No. US20050266443A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3589, 1015-003
; CURRENT APPLICATION NUMBER: US/11/093,746A
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: PCT/US2003/032270
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/417,842
; PRIOR FILING DATE: 2002-10-11

; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-093-746A-15

Query Match 6.7%; Score 44.4; DB 7; Length 591;
Best Local Similarity 47.2%; Pred. No. 1.4e-05;
Matches 169; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

Qy 85 AGAAGAGGCAAAATCTCTGTTCTGCTGCTGCAATGCTGGCAGACTACTCTTCG 144
Db 29 AGCGGAAACCCAGTGTGATGATGATGATGATGATGATGATGATGATGATG 88
Qy 145 ACATGCTCAGATGAGAGAACTGGGGCAATCAACCAACGAGTATCCAACTCAGAG 204
Db 89 ACAGCTGAAGGGCCACAGCTGTGAGAGACCTGCCACTGTGTTCACAGTGAAGC 148
Qy 205 AGTTGATATCAAG--AGTGAAGTTCAAGATTCGATCTGCTGCTGCTGCTG 261
Db 149 CTCTGAAGCTCTCTGCGGACGCTGCACTGCTCTGAGACGTTGGGGGAGGCCCCG 208
Qy 262 CTCGACGCTGTGAGAGGACTACTATGATGATGATGATGATGATGATGATG 321
Db 209 TCAGAGCCAGCTGAGAGGACTATGATGAGAGGACAGATATCTCTGTACGTCTG 268
Qy 322 CAGTGAAGAGGAGAGATTTGCTGAGTCAAGAAAGAGCTGATTTCTTCTCTG 381
Db 269 GCACAGATGAAGGCCGCTTACCGAGTGGGGCTGAGCTCAGAGAAAGTCTGAACG 328
Qy 382 ATTTCTGTGCCAAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 439
Db 329 CCAAGTGGCTGGCGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 386

RESULT 7
US-11-093-746A-1
; Sequence 1, Application US/11093746A
; Publication No. US20050266443A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3589, 1015-003
; CURRENT APPLICATION NUMBER: US/11/093,746A
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: PCT/US2003/032270
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/417,842
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3791
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-093-746A-1

Query Match 6.7%; Score 44.4; DB 7; Length 3791;
Best Local Similarity 47.2%; Pred. No. 4.1e-05;
Matches 169; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

Qy 85 AGAAGAGGCAAAATCTCTGTTCTGCTGCTGCAATGCTGGCAGACTACTCTTCG 144
Db 364 AGCGGAAACCCAGTGTGATGATGATGATGATGATGATGATGATGATGATG 423
Qy 145 ACATGCTCAGATGAGAGAACTGGGGCAATCAACCAACGAGTATCCAACTCAGAG 204
Db 424 ACAGCTGAAGGGCCACAGCTGTGAGAGACCTGCCACTGTGTTCACAGTGAAGC 483

Qy	205	AGTTGAGTATCAACAG---AGTGAAGTTCAAAAGCATTCGGATCGGCACACAATTCG	261
Db	484	CTGTGAAAGTCCCTGGGACAGTGTCACTACACTCTCTCTGGGACGTTGGGGGCGAGGCCGCCG	543
Qy	262	CTCGACGCGTGTGGAGGGACTACTATGCTAAAGTGAGTGTATAGTGTATCTCGTCACG	322
Db	544	TCAGACGACAGCTGGAAAGCACTATCTGGAAAGGCACAGATATCTCTGTATACGTCGTGGACA	603
Qy	322	CAGTAGACAGGGAGAAATTGCTGAGTGAABAAAGAGCTGATCTCTTCTCTCGACG	381
Db	604	GCAACAGTGAAGCCCGCTTACCCGAGTCGGCGGCTGAGCTACACAGAACTCTGAAACGACC	663
Qy	382	ATTCTCTGATCCCAAGTTCCTGTGCTGTGCTCTGGGAAAACAATTGATATCCCGTACGC	439
Db	664	CCAACTATGCTGGCGTCCCTCTTGTGTGTCTGCGCAACAGACGAGGACCTGATGCG	721

```

RESULT 8
US-10-750-185-28179
; Sequence 28179, Application US/10750185
; Publication No. US2005026063A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28179
; LENGTH: 676
; TYPE: DNA
; ORGANISM: Bovine 1986680693146
US-10-750-185-28179

```

[illegible]

```

RESULT 9
US-10-750-185-46137
; Sequence 46137, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482

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? PRIOR FILING DATE: 2002-12-31
 ? NUMBER OF SEQ ID NOS: 64922
 ? SOFTWARE: PatentIn version 3.1
 ? SEQ ID NO: 46137
 ? LENGTH: 976
 ? TYPE: DNA
 ? ORGANISM: Bovine
 ? OS-10-750-185-46137

Query Match	5.1k	Score 33.8	DB 6	Length 976
Beat Local Similarity	50.3k	Pred. No. 0.1		
Matches	83	Conservative	0	Mismatches 82
			Indels	0
			Gaps	0
Qy	218	CAGAGTGAAGTTCAAAGCATTCGATTCGGGTGGCCACACATCGCTCGACCGGTGTGGAG	277	
Db	811	CAGATTCGAGGTGAACATTTGGATGTGGGGCGGCAGAAAGTCCCTCGAGTCTTACTGCGC	870	
Qy	278	GGACTTACTATGCTAAGTGTGCTATATAGTATATCTGTCCAGCCGATGAGCAGGAGAG	337	
Db	871	GAATCTACTTTGAGAGCACCGACGGCCTCATCTTGGGTGTGGACAGCGCCGACCGCAGC	930	
Qy	338	ATTGTGTAGTCAAAGAAAGAGCTCGATTCCTCTCTCCGACGA	382	
Db	931	CATGACAGACTGCCAGCGGAGCTCTCAAAACCTGTGTGTGAGAGA	975	

```

RESULT 10
US-10-750-185-58595
Sequence 58595, Application US/10750185
Publication No. US2005026063A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MW1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58595
LENGTH: 1424
TYPE: DNA
ORGANISM: Bovine
US-10-750-185-58595
19866881395308

```

	Query Match	Similarity	4.9%	Score 33	DB 6	Length 1424	
	Best Local	Similarity	47.4%	Pred. No. 0.25			
	Matches	99	Conservative	0	Mismatches	110	Indels 0; Gaps 0
Qy	150	CTCAGAGTGAACA	CTGGGCAACATCA	CCACGACGATTC	CAACGTGAGGAGTTG	209	
Db	950	CTGAGGTCTCGA	AATATGGTTAAAC	CTTAAGAAAGTAGT	GAATCTCCAAACAGTCA	1001	
Qy	210	AGATTCACA	CAGAGGAAGTCA	AAAGCATTCGAT	CTGGGTGGCCACACAT	GCCTGACGC	269
Db	1010	AATCTCGAAGG	CTACCTCTTGAC	CAAGAGAAAGATTT	TATATCTCTCTTAATTT	1061	
Qy	270	GTGTGAGGGA	CTACTATGCTA	AGGTGATGCTAT	ATGTATCTGTG	CGACGACAGTAAC	329
Db	1070	GAATATTGGG	CTAACTTTAA	AAATATGATG	GAACCTGAAAC	CTCAATATCTTTGGGCAC	1124
Qy	330	AGGAGAGATT	TTGCTGAGT	CAAAAGAAA		358	
Db	1130	CTGATGTGA	AGAGCTAACT	CAATTTGAAAA		1158	

RESULT 11
US-10-750-185-62691/c
; Sequence 62691, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62691
; LENGTH: 1613
; TYPE: DNA
; ORGANISM: Bovine 1986680920645
US-10-750-185-62691

Query Match 4.9%; Score 33; DB 6; Length 1613;
Best Local Similarity 57.1%; Pred. No. 0.27;
Matches 60; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Qy 544 TGTGCAATTTGCGCAAAATGGGTACGTTTCAAGTGATGACCAATGACA 603
Db 1065 TGTTAATGTTGTTGCTTAATTCAGGGCGGTGGAGTAGATGACAGAAATAGTTCA 1006
Qy 604 TCAAGTATTTCTTCTGTGAAAGAGAACTTAGCTCGGTGTT 648
Db 1005 TCAAGTATTTTATTTCTTTTAAAAAGAACTGTGTGGGTTT 961

RESULT 12
US-10-750-185-38735
; Sequence 38735, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38735
; LENGTH: 1994
; TYPE: DNA
; ORGANISM: Bovine 198668081805084
US-10-750-185-38735

Query Match 4.9%; Score 32.6; DB 6; Length 1994;
Best Local Similarity 51.7%; Pred. No. 0.42;
Matches 74; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 365 TTCTCTCTCCGACGATTTCTGTCCCAAGTTCTGTGCTGCTCTGGGAAACAAGAT 424
Db 973 TTTATGTTCTTCAAAATAGCATCTGTCCACAGATGCTGTGCTTCCCTGGCGCTCAGA 1032

Qy 425 TGATATCCGTCAGCTTCTTGTGAAGACGATTCGCTTCACTTGATGACATGAC 484
Db 1033 TGTTAAGATCTGCTTGAATGAGGAGTCTTGAATTTGATCTCCGGTGGGAAGATC 1092
Qy 485 CACTGTAAAGAACGTTGAACC 507
Db 1093 CCTGTGATGAGAAATGCAAAAC 1115

RESULT 13
US-10-750-185-255/c
; Sequence 255, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 255
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine MM8T08970
US-10-750-185-255

Query Match 4.8%; Score 32.2; DB 6; Length 600;
Best Local Similarity 55.2%; Pred. No. 0.29;
Matches 58; Conservative 2; Mismatches 45; Indels 0; Gaps 0;

Qy 544 TGTGCAATTTGCGCAAAATGGGTACGTTTCAAGTGATGACCAATGACA 603
Db 409 TGTTAATGTTGCTTAAATTCAGGGCGGTGGAGTAGATGACAGAAATAGTTCA 350
Qy 604 TCAAGTATTTCTTCTGTGAAAGAGAACTTAGCTCGGTGTT 648
Db 349 TCAAGTATTTTATTTCTTTTAAAAAGAACTGTGTGGGTTT 305

RESULT 14
US-10-750-185-47498/c
; Sequence 47498, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47498
; LENGTH: 2140
; TYPE: DNA
; ORGANISM: Bovine 1986680489188
US-10-750-185-47498

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 00:07:31 ; Search time 134 Seconds

(without alignments)
629.558 Million cell updates/sec

Title: US-10-688-481-11

Sequence: 1 MFLVDMFYGFGLASIGLWQKE.....SIVRKMGYGEGRFMNTQYIK 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq.21.*
1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	998	100.0	192	5	ABB81583 Physcomit
2	998	100.0	192	8	ADT91574 Physcomit
3	880.5	88.2	225	8	ADY22898 Plant ful
4	880.5	88.2	229	8	ADY23452 Plant ful
5	880.5	88.2	236	8	ADY05691 Plant ful
6	867.5	86.9	255	8	ADY08914 Plant ful
7	866.5	86.8	193	7	ABM74047 DNA clone
8	862.5	86.4	193	3	AAG30108 Arabidops
9	862.5	86.4	208	8	ABG59985 Human DIT
10	862.5	86.4	208	8	ADX88378 Plant ful
11	862.5	86.4	236	8	ADY07438 Plant ful
12	862.5	86.4	244	8	ADY07420 Plant ful
13	862.5	86.4	251	8	ADX87922 Plant ful
14	862.5	86.4	280	8	ADY10442 Plant ful
15	859.5	86.1	266	8	ADY75842 Plant ful
16	851.5	85.3	191	3	AAG30109 Arabidops
17	850.5	85.2	193	3	AAG15475 Arabidops
18	842.5	84.4	292	3	AAG35214 Zea mays
19	842.5	84.4	300	3	AAG35213 Zea mays
20	842.5	84.4	305	3	AAG35212 Zea mays
21	822.5	82.4	193	3	AAG30994 Arabidops
22	674.5	67.6	193	4	ABB62939 Drosophila
23	671.5	67.3	155	3	AAG30110 Arabidops
24	660.5	66.2	155	3	AAG15476 Arabidops

25	649.5	65.1	155	3	AAG30995 Arabidops
26	627	62.8	189	6	ABJ25768 Apeyrg11
27	615	61.6	189	6	ABJ26368 Apeyrg11
28	615	61.6	199	9	ADY64776 S. mansoni
29	614.5	61.6	198	2	AAW74176 Human GTP
30	614.5	61.6	198	2	AAW74176 Human GTP
31	614.5	61.6	198	4	AAW74177 Human SAR
32	614.5	61.6	198	4	AAW74178 Chinese h
33	614.5	61.6	198	8	ADY020049 Human PRO
34	614.5	61.6	198	8	ADP55234 Human PRO
35	614.5	61.6	198	8	ADP24917 PRO polyp
36	614.5	61.6	199	2	AAW74864 Human sec
37	614.5	61.6	199	2	AAW74864 Human nov
38	614.5	61.6	199	6	ABO34509 Region of
39	614.5	61.6	199	7	ADY23170 Novel hum
40	614.5	61.6	199	8	ADH74172 Human sec
41	613.5	61.5	190	5	ABP73936 Candida
42	606.5	60.8	190	4	ABG70914 S cerevis
43	605.5	60.7	198	8	ADY32522 Arabid
44	600.5	60.2	198	8	ADY32526 Mutant Sa
45	600.5	60.2	198	8	ADY32530 Mutant Sa

ALIGNMENTS

RESULT 1
ABB81583
ID ABB81583 standard; protein; 192 AA.
XX
AC ABB81583;
XX
DT 18-SEP-2002 (first entry)
XX
DE Physcomitrella patens GBP-1 protein sequence SEQ ID NO:11.
XX
XX Physcomitrella patens; GBP; GTP binding protein; GBSRP; plant;
XX GTP binding stress-related protein; transgenic plant; agricultural;
XX environmental stress; salinity; drought; temperature.
XX
XX Physcomitrella patens.
XX
OS US2002066124-A1.
XX
PN 30-MAY-2002.
PD
XX
XX 06-APR-2001; 2001US-00828310.
XX
XX 07-APR-2000; 2000US-0196001P.
XX
XX (SILV/) SILVA O D C E.
XX (BOHN/) BOHNERT H J.
XX (THIE/) THIELEN N V.
XX (CHEN/) CHEN R.
XX
XX Silva ODCE, Bohnert HJ, Thielen NV, Chen R;
XX WPI; 2002-556781/59.
XX N-PSDB; ABB81583.
XX
XX Novel GTP binding stress-related proteins and genes encoding the
XX proteins, useful for producing transgenic plants having increased
XX tolerance to environmental stress as compared to wild type variety of
XX plant cell.
XX
XX Claim 14; Fig 3A; 73pp; English.
XX
XX The present invention describes an isolated GTP binding stress-related
XX protein (GBSRP) (I) from Physcomitrella patens, selected from GTP binding
XX protein-1 (GBP-1), GBP-2, GBP-3, GBP-4 and GBP-5, or its orthologues. (I)
XX can be used for producing a transgenic plant (e.g. maize, wheat, rice,
XX oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola,
XX manihot, pepper, sunflower, tagetes, solanaceous plants, potato, tobacco,

CC eggplant, tomato, vicia species, pea, alfalfa, coffee, cacao, tea, Salix
CC species, oil palm, coconut, perennial grass and forage crops). The
CC transgenic plants produced have increased tolerance to environmental
CC stress (e.g. salinity, drought and temperature) as compared to a wild
CC type variety of the plant, from the plant cell. GBSRP polynucleotide
CC sequences can be used as markers for specific regions of the genome, and
CC also in functional studies of P. patens proteins. They can also be used
CC for evolutionary and protein structural studies. The present sequence
CC represents the P. patens GBP-1 protein, which is used in the
CC exemplification of the present invention
XX

XX Sequence 192 AA;

Query Match 100.0%; Score 998; DB 5; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.4e-106;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFLVDMFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQYPTSEELS 60
DB 1 MFLVDMFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQYPTSEELS 60
QY 61 INRYKFAFDLGGHTTARRWRDYYAKVDALVYLVDVDRERFAESKKEIDSLSDSLS 120
DB 61 INRYKFAFDLGGHTTARRWRDYYAKVDALVYLVDVDRERFAESKKEIDSLSDSLS 120
QY 121 QVPLVLGNKIDIPYASSEDELRFLLGLTWTGKGVNLGDSNIRPIEVFMCIVRMGY 180
DB 121 QVPLVLGNKIDIPYASSEDELRFLLGLTWTGKGVNLGDSNIRPIEVFMCIVRMGY 180
QY 181 GEGFKMNTQYIK 192
DB 181 GEGFKMNTQYIK 192

RESULT 2

ID ADT91574 standard; protein; 192 AA.

XX ADT91574;

XX 16-DEC-2004 (first entry)

XX Physcomitrella patens GTP binding protein, PgGBP-1.

XX GTP-binding stress-related protein; GBSRP; transgenic plant;

XX environmental stress tolerance; stress resistance; cell metabolism;

XX GTP binding protein; GBP.

XX Physcomitrella patens.

XX US2004194163-A1.

XX 30-SEP-2004.

XX 17-OCT-2003; 2003US-00688481.

XX 07-APR-2000; 2000US-0196001P.

XX 06-APR-2001; 2001US-00828310.

XX (BADI) BASF PLANT SCI GMBH.

XX Da Costa E SilvaO, Bohner HJ, Thielén NV, Chen R;

XX MPI; 2004-698822/68.

XX N-PSDB; ADT91569.

XX Novel isolated nucleic acid encoding polypeptide e.g., GTP-binding stress

XX -related protein, useful for producing vector utilized for producing

XX transgenic plant that has increased tolerance to environmental stress.

XX Example 6; SEQ ID NO 11, 62pp; English.

CC stress-related proteins (GBSRP). GBSRP DNA is useful for producing a
CC recombinant expression vector utilized for producing a transgenic plant
CC that has increased tolerance to environmental stress, for identifying and
CC Physcomitrella patens and related organisms, for identifying and
CC localising P. patens sequences of interest, for evolutionary studies, for
CC determining GBSRP regions required for function, for modulating GBSRP
CC activity, for modulating metabolism of one or more cell function, for
CC modulating transport of one or more compounds, for modulating stress
CC resistance or as markers for specific regions of the genome of P. patens.
CC The present sequence is the Physcomitrella patens GTP binding protein
CC (GBP).
XX

XX Sequence 192 AA;

Query Match 100.0%; Score 998; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.4e-106;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFLVDMFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQYPTSEELS 60
DB 1 MFLVDMFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQYPTSEELS 60
QY 61 INRYKFAFDLGGHTTARRWRDYYAKVDALVYLVDVDRERFAESKKEIDSLSDSLS 120
DB 61 INRYKFAFDLGGHTTARRWRDYYAKVDALVYLVDVDRERFAESKKEIDSLSDSLS 120
QY 121 QVPLVLGNKIDIPYASSEDELRFLLGLTWTGKGVNLGDSNIRPIEVFMCIVRMGY 180
DB 121 QVPLVLGNKIDIPYASSEDELRFLLGLTWTGKGVNLGDSNIRPIEVFMCIVRMGY 180
QY 181 GEGFKMNTQYIK 192
DB 181 GEGFKMNTQYIK 192

RESULT 3

ID ADY22898 standard; protein; 225 AA.

XX ADY22898;

XX 21-APR-2005 (first entry)

XX Plant full length insert polypeptide seqid 70682.

XX plant protectant; plant growth regulant; gene therapy; plant;

XX recombinant DNA construct; physical array; plant breeding marker;

XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

XX extreme osmotic condition; pathogen tolerance; pest tolerance;

XX growth rate; cell cycle pathway; disease resistance;

XX galactomanan production; lignin production; plant growth regulator;

XX yield; plant growth; plant development; seed oil; protein yield;

XX protein content.

XX Unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

XX 05-NOV-2001; 2001US-00985678.

XX (LIU/) LIU J.

XX (ZHOU/) ZHOU Y.

XX (KOVA/) KOVALIC D K.

XX (SCRE/) SCREEN S E.

XX (TABAS/) TABASKA J E.

XX (CAOY/) CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

AC ADY05691;
XX
XX 21-APR-2005 (first entry)
XX
DE plant full length insert polypeptide seqid 61506.
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
KM recombinant DNA construct; physical array; plant breeding marker;
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KM extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KM galactomannan production; lignin production; plant growth regulator;
KM yield; plant growth; plant development; seed oil; protein yield;
KM protein content.
XX
XX Unidentified.
XX
XX US2004034888-A1.
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
XX 05-NOV-2001; 2001US-00985678.
XX
XX (LIU/J) LIU J.
XX (ZHOU/J) ZHOU Y.
XX (KOVA/) KOVALIC D K.
XX (SCRE/) SCREEN S E.
XX (TABA/) TABASKA J E.
XX (CAOY/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 61506; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.
XX
XX Sequence 236 AA;
SQ
Query Match 88.2%; Score 880.5; DB 8; Length 236;
Best Local Similarity 84.5%; Pred. No. 7.3e-93;
Matches 163; Conservative 19; Mismatches 10; Indels 1; Gaps 1;
QY 1 MFVDMVFYGLASIGLWQKAKITLFLGDNAGKTTLLHMLKDEKXGQHPTQYPTSESL 60
DB 44 MFVDMVFYGLASIGLWQKAKITLFLGDNAGKTTLLHMLKDEKXGQHPTQYPTSESL 103

QY 61 INRVKFAEDLGSHITARRVRYDYAKVDALVYLVDAVDRERFAESKKEIDSLSDSLS 120
DB 104 IGRIFKFAFDLGGHQIARRVWKDYAKVDVVYLVDAVDRERFAESKKEIDALLDLSLA 163
QY 121 QVPEVLVGNKIDIPVASSDEBELRFTLGLT-MTNGKGTNVLGDSNIRPIEFMCSYRXMG 179
DB 164 NVPEFLITGNKIDIPVASSBELRYVGLSNFTTGKGVNLADSNVRPLEIFMCSVVRKMG 223
QY 180 YGSGFKMPTQYIK 192
DB 224 YGSGFKMMSGYIK 236
RESULT 6
ADY08914
ID ADY08914 standard; protein; 255 AA.
XX
XX ADY08914;
XX
XX 21-APR-2005 (first entry)
XX
XX DE plant full length insert polypeptide seqid 64729.
XX
XX KM plant protectant; plant growth regulant; gene therapy; plant;
KM recombinant DNA construct; physical array; plant breeding marker;
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KM extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KM galactomannan production; lignin production; plant growth regulator;
KM yield; plant growth; plant development; seed oil; protein yield;
KM protein content.
XX
XX Unidentified.
XX
XX OS US2004034888-A1.
XX
XX PN 19-FEB-2004.
XX
XX PD 28-APR-2003; 2003US-00425114.
XX
XX PF 06-MAY-1999; 99US-00304517.
XX 05-NOV-2001; 2001US-00985678.
XX
XX (LIU/J) LIU J.
XX (ZHOU/J) ZHOU Y.
XX (KOVA/) KOVALIC D K.
XX (SCRE/) SCREEN S E.
XX (TABA/) TABASKA J E.
XX (CAOY/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 64729; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of

CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.

XX Sequence 255 AA;

Query Match 86.9%; Score 867.5; DB 8; Length 255;

Best Local Similarity 83.4%; Pred. No. 2.6e-91;
Matches 161; Conservative 19; Mismatches 12; Indels 1; Gaps 1;

QY 1 MFLVDMFYGFVLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGHOHPTQPTSEELS 60
DB 63 MFLVDMFYGVLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVQHPTQPTSEELS 122
QY 61 INRVKFAFDLGGHTTARRVWRDYAKVDAIVLVDAVDEREPFAESKKEIDSLSDSL 120
DB 123 IGRKFKAFDLDGGHQTARRVWKDYAKVDAVVYLVDVDEREPFAESKKEIDALLADSLA 182
QY 121 QVPVLVGNKIDIPYASSEDELRFTLGLT-MTTGKGTNLDGSDNIRPIEVFMC SIYRKMG 179
DB 183 NVFPLITGNKIDIPYASSEELRYHGLSNFTTGKGVNLADSNVRPLEIFMCSIVYRKMG 242
QY 180 YGEGFKMTQYIK 192
DB 243 YGEGFKMTSQYIK 255

RESULT 7

ABM74047
ID ABM74047 standard; protein; 193 AA.

XX AC ABM74047;

DT 17-OCT-2003 (first entry)

XX DNA clone originating in barley containing SNP sequence #457.

XX Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.

XX OS Hordeum vulgare.

XX PN W02003057877-A1.

XX PD 17-JUL-2003.

XX PF 16-DEC-2002; 2002WO-IB005403.

XX PR 20-DEC-2001; 2001JP-00387059.

XX PR 20-DEC-2001; 2001JP-00387131.

XX PR 20-DEC-2001; 2001JP-00403299.

XX PR 20-DEC-2001; 2001JP-00403300.

XX PR 27-SEP-2002; 2002JP-00327515.

XX PA (UTNT-) UNIV JAPAN OKAYAMA.

XX PI Sato K, Takeda K, Kohara Y;

XX DR WPI; 2003-587127/55.

XX PT Single nucleotide polymorphism sites in barley varieties and DNA

XX PT sequences containing them for analysis and identification of barley

XX PT characteristics and production of barley transformants with desired

XX PT characteristics.

XX PS Disclosure; SEQ ID XX; 284bp; Japanese.

XX CC The present invention relates to oligonucleotide clones originating in

CC CC barley (Hordeum vulgare) which contain single nucleotide polymorphisms

CC CC (SNP). The oligonucleotides may be used for analysis of SNPs among barley

CC CC varieties, identification of particular varieties and genotype-phenotype

CC analysis, isolation of specific genes and creation of new varieties by
CC transformation of barley varieties with them and production of new barley
CC varieties with desired properties. The present sequence represents an
CC oligonucleotide clone sequence featured in the specification. The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published-pct-sequences

XX Sequence 193 AA;

Query Match 86.8%; Score 866.5; DB 7; Length 193;

Best Local Similarity 83.9%; Pred. No. 2.3e-91;
Matches 162; Conservative 19; Mismatches 11; Indels 1; Gaps 1;

QY 1 MFLVDMFYGFVLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGHOHPTQPTSEELS 60
DB 1 MFLVDMFYGVLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVQHPTQPTSEELS 60
QY 61 INRVKFAFDLGGHTTARRVWRDYAKVDAIVLVDAVDEREPFAESKKEIDSLSDSL 120
DB 61 IGRKFKAFDLDGGHQTARRVWKDYAKVDAVVYLVDVDEREPFAESKKEIDALLADSLA 120
QY 121 QVPVLVGNKIDIPYASSEDELRFTLGLT-MTTGKGTNLDGSDNIRPIEVFMC SIYRKMG 179
DB 121 TVFPLITGNKIDIPYASSEELRYHGLSNFTTGKGVNLADSNVRPLEIFMCSIVYRKMG 180
QY 180 YGEGFKMTQYIK 192
DB 181 YGEGFKMTSQYIK 193

RESULT 8

AAG30108
ID AAG30108 standard; protein; 193 AA.

XX AC AAG30108;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 35936.

XX Protein identification; signal transduction pathway; metabolic pathway;

XX KM hybridisation assay; genetic mapping; gene expression control; promoter;

XX KM termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

XX PR 05-MAR-1999; 99US-0123180P.

XX PR 09-MAR-1999; 99US-0123548P.

XX PR 23-MAR-1999; 99US-0125788P.

XX PR 29-MAR-1999; 99US-0126264P.

XX PR 01-APR-1999; 99US-0126785P.

XX PR 06-APR-1999; 99US-0128234P.

XX PR 08-APR-1999; 99US-0128714P.

XX PR 16-APR-1999; 99US-0129845P.

XX PR 21-APR-1999; 99US-0130077P.

XX PR 23-APR-1999; 99US-0130510P.

XX PR 23-APR-1999; 99US-0130891P.

XX PR 28-APR-1999; 99US-0131449P.

XX PR 30-APR-1999; 99US-0132048P.

XX PR 04-MAY-1999; 99US-0132407P.

XX PR 05-MAY-1999; 99US-0132484P.

XX PR 06-MAY-1999; 99US-0132485P.

XX PR 06-MAY-1999; 99US-0132486P.

PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135628P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.

PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 25-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 08-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149930P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 25-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154038P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 26-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156569P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159684P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.

CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.

XX Sequence 236 AA;

Query Match Best Local Similarity 86.4%; Score 862.5; DB 8; Length 236;
 Matches 160; Conservative 21; Mismatches 11; Indels 1; Gaps 1;

QY 1 MFLVDFVYGLASIGLMOKEAKILFLGLDNAGKTTLLHMLKDEKLGHOPTQYPTSEELS 60
 DB 44 MFLMDVYVGLASIGLMOKEAKILFLGLDNAGKTTLLHMLKDEKLGHOPTQYPTSEELS 103
 QY 61 INRVKFAFDLGHTTARRVWRDYAKVDAIVYLVDVAVRERPAESKKEIDSLSDSLA 120
 DB 104 IGIKFKFAPDLGGHQIARRVWKDYAKVDAVVYLVDAVDEREPAESKKEIDALLSDSLA 163
 QY 121 QVPVLVIGNKIDIPYASSEDELRFITGLT-MTTGKGTVMNGDSNIRPIEFVFMCSIVRKMG 179
 DB 164 NVFPLIGNKIDIPYASSEBELRYHGLSNFTTGKGVNLGDSNVRLPLEVFMCSIVRKMG 223
 QY 180 YGEGFKMWTQYIK 192
 DB 224 YGDGFKMWSQYIK 236

RESULT 12
 ID ADY07420 standard; protein; 244 AA.

AC ADY07420;
 DT 21-APR-2005 (first entry)

XX Plant full length insert polypeptide seqid 63235.

KM plant protectant; plant growth regulant; gene therapy; plant;
 KM recombinant DNA construct; physical array; plant breeding marker;
 KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KM extreme osmotic condition; pathogen tolerance; pest tolerance;
 KM growth rate; cell cycle pathway; disease resistance;
 KM galactomannan production; lignin production; plant growth regulator;
 KM yield; plant growth; plant development; seed oil; protein yield;
 KM protein content.

XX Unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX 26-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.
 XX 05-NOV-2001; 2001US-00985678.

PA (LITU/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABAA/) TABASKA J E.
 PA (CAOV/) CAO Y.

PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for

PT improving yield.

XX Claim 1; SEQ ID NO 63235; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.

XX Sequence 244 AA;

Query Match Best Local Similarity 86.4%; Score 862.5; DB 8; Length 244;
 Matches 160; Conservative 21; Mismatches 11; Indels 1; Gaps 1;

QY 1 MFLVDFVYGLASIGLMOKEAKILFLGLDNAGKTTLLHMLKDEKLGHOPTQYPTSEELS 60
 DB 52 MFLMDVYVGLASIGLMOKEAKILFLGLDNAGKTTLLHMLKDEKLGHOPTQYPTSEELS 111
 QY 61 INRVKFAFDLGHTTARRVWRDYAKVDAIVYLVDVAVRERPAESKKEIDSLSDSLA 120
 DB 112 IGIKFKFAPDLGGHQIARRVWKDYAKVDAVVYLVDAVDEREPAESKKEIDALLSDSLA 171
 QY 121 QVPVLVIGNKIDIPYASSEDELRFITGLT-MTTGKGTVMNGDSNIRPIEFVFMCSIVRKMG 179
 DB 172 NVFPLIGNKIDIPYASSEBELRYHGLSNFTTGKGVNLGDSNVRLPLEVFMCSIVRKMG 231
 QY 180 YGEGFKMWTQYIK 192
 DB 232 YGDGFKMWSQYIK 244

RESULT 13
 ID ADX87922 standard; protein; 251 AA.

AC ADX87922;

DT 21-APR-2005 (first entry)

XX Plant full length insert polypeptide seqid 50586.

KM plant protectant; plant growth regulant; gene therapy; plant;
 KM recombinant DNA construct; physical array; plant breeding marker;
 KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KM extreme osmotic condition; pathogen tolerance; pest tolerance;
 KM growth rate; cell cycle pathway; disease resistance;
 KM galactomannan production; lignin production; plant growth regulator;
 KM yield; plant growth; plant development; seed oil; protein yield;
 KM protein content.

XX Unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX 26-APR-2003; 2003US-00425114.

PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
XX (LIU/J.) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAS/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SF, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 50586; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.
XX
XX Sequence 251 AA;
SQ
Query Match 86.4%; Score 862.5; DB 8; Length 251;
Best Local Similarity 82.9%; Pred. No. 9.7e-91;
Matches 160; Conservative 21; Mismatches 11; Indels 1; Gaps 1;
QY 1 MFLVDMFYGFPLASISGLMOKKAKILFLGLDNAGKTTLLHMLKDEKLGQHPTQPTSEELS 60
DB 59 MFLMDMFYGVLASISGLMOKKAKILFLGLDNAGKTTLLHMLKDBRLVQHPTQPTSEELS 118
QY 61 INRVKFAFDLGGHTIARRVWDYAKVDAIVYLVDADVDRERFAESKKELDLSDLSLS 120
DB 119 IGIKIKFAFDLGGHGIARRVWKDYAKVDAIVYLVDADVDRERFAESKKELDLSDLSLS 178
QY 121 QVPVLVGNKIDIPYASSEBELRFTLGLT-MTTGKGTVNLGDSNIRPIEVNCSIVYKMG 179
DB 179 NVPFILGNKIDIPYASSEBELRYHGLSNFTTGKGTVNLGDSNIRPIEVNCSIVYKMG 238
QY 180 YGEGFKMTTOYIK 192
DB 239 YGDGFKMWSOYIK 251
XX
XX RESULT 14
XX ADY10442
XX ID ADY10442 standard; protein; 280 AA.
XX
XX ADY10442;
AC
XX 21-APR-2005 (first entry)
DT
XX Plant full length insert polypeptide seqid 66257.
DE
XX

KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content.
XX
XX Unidentified.
XX
XX US2004034888-A1.
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
XX 05-NOV-2001; 2001US-00985678.
XX
XX (LIU/J.) LIU J.
XX (ZHOU/) ZHOU Y.
XX (KOVA/) KOVALIC D K.
XX (SCRE/) SCREEN S E.
XX (TABAS/) TABASKA J E.
XX (CAOY/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SF, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 66257; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.
XX
XX Sequence 280 AA;
SQ
Query Match 86.4%; Score 862.5; DB 8; Length 280;
Best Local Similarity 82.9%; Pred. No. 1.1e-90;
Matches 160; Conservative 21; Mismatches 11; Indels 1; Gaps 1;
QY 1 MFLVDMFYGFPLASISGLMOKKAKILFLGLDNAGKTTLLHMLKDEKLGQHPTQPTSEELS 60
DB 88 MFLMDMFYGVLASISGLMOKKAKILFLGLDNAGKTTLLHMLKDBRLVQHPTQPTSEELS 147
QY 61 INRVKFAFDLGGHTIARRVWDYAKVDAIVYLVDADVDRERFAESKKELDLSDLSLS 120
DB 148 IGIKIKFAFDLGGHGIARRVWKDYAKVDAIVYLVDADVDRERFAESKKELDLSDLSLS 207
QY 121 QVPVLVGNKIDIPYASSEBELRFTLGLT-MTTGKGTVNLGDSNIRPIEVNCSIVYKMG 179
XX

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 01:13:16 ; Search time 38 Seconds
(without alignments)
486.148 Million cell updates/sec

Title: US-10-688-481-11

Perfect score: 998
Sequence: 1 MFLVDMFYGLASIGLMQKE.....SIVRKMGYGEGRKMTQYIK 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: PIR 80: *
2: PIR1: *
3: PIR2: *
4: PIR3: *
5: PIR4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	871.5	87.3	193	2 T52096	small GTP-binding
2	863.5	86.5	193	2 S42528	GTP-binding protei
3	862.5	86.4	193	2 T01509	GTP-binding protei
4	854.5	85.6	193	2 T16964	GTP-binding protei
5	850.5	85.2	193	2 S28603	GTP-binding protei
6	848.5	85.0	193	2 T52094	small GTP-binding
7	843.5	84.5	193	2 T52095	ras-like small mon
8	835.5	83.7	193	2 T16993	GTP-binding protei
9	832	83.4	194	2 T16966	GTP-binding protei
10	822.5	82.4	193	2 DB6224	hypothetical prote
11	706	70.7	198	2 T03696	GTP-binding protei
12	628.5	63.0	190	2 S28605	GTP-binding protei
13	625	62.6	190	2 S71588	GTP-binding protei
14	593.5	59.5	193	2 T29706	GTP-binding protei
15	585.5	58.7	198	2 S39543	GTP-binding protei
16	562	56.3	190	2 A33619	GTP-binding protei
17	521	52.2	111	2 S71589	GTP-binding protei
18	297.5	29.8	190	2 T09136	ADP-riboylation f
19	277.5	27.8	184	2 T21126	ADP-riboylation f
20	275	27.6	181	2 A54022	ADP-riboylation f
21	274	27.5	180	2 T22655	ADP-riboylation f
22	271.5	27.2	182	2 B54869	ADP-riboylation f
23	271.5	27.2	183	2 S46035	ADP-riboylation f
24	270	27.1	180	2 A40438	GTP-binding protei
25	269.5	27.0	182	2 A54869	ADP-riboylation f
26	267.5	26.8	182	2 S41938	ADP-riboylation f
27	261	26.2	175	2 T31519	ADP-riboylation f
28	259.5	26.0	175	4 I50632	hypothetical CPs1
29	257.5	25.8	175	2 B23741	ADP-riboylation f

30	257.5	25.8	175	2 JC4950	ADP-riboylation f
31	253	25.4	183	2 D49993	ADP-riboylation f
32	250.5	25.1	180	2 T32978	ADP-riboylation f
33	250.5	25.1	191	2 S29608	ADP-riboylation f
34	250	25.1	182	2 C49993	ADP-riboylation f
35	249.5	25.0	175	2 B53859	ADP-riboylation f
36	248.5	24.9	179	2 JH0260	ADP-riboylation f
37	243.5	24.4	178	2 S40940	ADP-riboylation f
38	243.5	24.4	181	2 A36367	ADP-riboylation f
39	242.5	24.3	180	2 S37599	ADP-riboylation f
40	242.5	24.3	181	2 B36167	ADP-riboylation f
41	241.5	24.2	182	2 T52341	ADP-riboylation f
42	241	24.1	182	2 A49520	ADP-riboylation f
43	240.5	24.1	181	2 A41570	ADP-riboylation f
44	240.5	24.1	181	2 T52339	ADP-riboylation f
45	240.5	24.1	181	2 S49325	ADP-riboylation f

ALIGNMENTS

RESULT 1
T52096
small GTP-binding protein Sar1Bnt [imported] - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C:Accession: T52096
R:Andreeva, A.V.; Kutzov, M.A.; Evans, D.E.; Hawes, C.R.
submitted to the EMBL Data Library, December 1999
A:Description: Plant proteins involved in membrane transport between the endoplasmic ret;
A:Reference number: 225950
A:Accession: T52096
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-193 <AND>
A:Cross-references: UNIPROT:Q9SD05; UNIPARC:UP100000ACFAF; EMBL:AF210431; PIDN:AAF17254.1
C:Superfamily: ADP-riboylation factor

Query Match 87.3%; Score 871.5; DB 2; Length 193;
Best Local Similarity 83.4%; Pred. No. 4.9e-69;
Matches 161; Conservative 21; Mismatches 10; Indels 1; Gaps 1;

QY	1	MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDBKLGCHQPTQYPTSELS	60
DB	1	MFLVDMFYGLATLGLMQEAKILFLGLDNAGKTTLLHMLKDBRLVQHQPPTSELS	60
QY	61	INRKRKAPDLGGHTIARRVWRDYAKVDAIVLVDAVDREFAESKKELDLSDSL	120
DB	61	IGRIKFAFDLGGHQIARRVWKDYAKVDAIVLVDSFDKRPFAESKKELDLSDSLA	120
QY	121	QVPLVLGNKIDIPYASSEBELAFTIGLT-MTGGKTVNLGDSNINPIEYFMCSIVRKMG	179
DB	121	TVPLFLGNKIDIPYASSEBELRYHMLTGVTTGKGVKNLADSNVRVEVFMCSIVRKMG	180
QY	180	YGEGRKMTQYIK 192	
DB	181	YGEGRKMTQYIK 193	

RESULT 2
S42528
GTP-binding protein SAR1 homolog - tomato
N:Alternate names: GTPase-like protein
C:Species: Lycopersicon esculentum (tomato)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S42528
R:Davies, C.
Plant Mol. Biol. 24, 525-531, 1994
A>Title: Cloning and characterization of a tomato GTPase-like gene related to yeast and J

A:Cross-references: UNIPROT:P52884; UNIPARC:UPI0000135564; EMBL:L12051; NID:g473683; PID:
C:Function:
A:Description: involved in vesicular transport
C:Superfamily: ADP-riboseylation factor
C:Keywords: GTP binding; nucleotide binding; P-loop
F:27-34/Region: nucleotide-binding motif A (P-loop)
F:129-132/Region: GTP-binding NKXD motif

Query Match 86.5%; Score 863.5; DB 2; Length 193;
Best Local Similarity 83.9%; Pred. No. 2.5e-68;
Matches 162; Conservative 16; Mismatches 14; Indels 1; Gaps 1;

QY 1 MFLVDMFYGFLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQYPTSEELS 60
DB 1 MFLVDMFYGFLASIGLMQKDKILFLGLDNAGKTTLLHMLKDEKLVQHOPQYPTSEELS 60

QY 61 INRVKFAFDLGGHTTARRVWRDYAKVDALVYLVDAVDRERFESKKEIDSLSDSL 120
DB 61 IGRKIKFAFDLGGHQAIRRVWRDYAKVDVAVYLVDAVDRERFESKKEIDSLSDSL 120

QY 121 QVPLVLTGNKIDIPYASSEDELRFTLGLT-MTTGKGVNLGDSNIRPIEVFMCISYVRKM 179
DB 121 NVPLIIGNKIDIPYASSEDELRVHLGLTGVTTGKGNINLAGTVVRPIEVFMCISYVRKM 180

QY 180 YGEGFKMVSQYIK 192
DB 181 YGEGFKMVSQYIK 193

RESULT 3
T01509
GTP-binding protein T10M13.9 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01509
R:Johnson, A.F.; de la Bastide, M.; Lodhi, M.; Hoffman, J.; Hasegawa, A.; Gnoj, L.; Gort
Martensen, R.; McCombie, W.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of the Arabidopsis thaliana T10M13 BAC.
A:Reference number: 214346
A:Accession: T01509
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-193 <JCH>
A:Cross-references: UNIPROT:O04834; UNIPARC:UPI000001457; EMBL:AF001308; NID:g2104523;
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4S
A:Intons: 43/3; 87/3
A>Note: T10M13.9
C:Superfamily: ADP-riboseylation factor
C:Keywords: GTP binding; nucleotide binding; P-loop
F:27-34/Region: nucleotide-binding motif A (P-loop)
F:129-132/Region: GTP-binding NKXD motif

Query Match 86.4%; Score 862.5; DB 2; Length 193;
Best Local Similarity 82.9%; Pred. No. 3e-68;
Matches 160; Conservative 21; Mismatches 11; Indels 1; Gaps 1;

QY 1 MFLVDMFYGFLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQYPTSEELS 60
DB 1 MFLVDMFYGFLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVQHOPQYPTSEELS 60

QY 61 INRVKFAFDLGGHTTARRVWRDYAKVDALVYLVDAVDRERFESKKEIDSLSDSL 120
DB 61 IGRKIKFAFDLGGHQAIRRVWRDYAKVDVAVYLVDAVDRERFESKKEIDSLSDSL 120

QY 121 QVPLVLTGNKIDIPYASSEDELRFTLGLT-MTTGKGVNLGDSNIRPIEVFMCISYVRKM 179
DB 121 NVPLIIGNKIDIPYASSEDELRVHLGLTGVTTGKGNINLAGTVVRPIEVFMCISYVRKM 180

QY 180 YGEGFKMVSQYIK 192
DB 181 YGEGFKMVSQYIK 193

DB 181 YGEGFKMVSQYIK 193

RESULT 4
T16964
GTP-binding protein - curled-leaved tobacco
C:Species: Nicotiana glauca (curled-leaved tobacco)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16964
R:Borjsek, N.
submitted to the EMBL Data Library, September 1996

Query Match 85.6%; Score 854.5; DB 2; Length 193;
Best Local Similarity 82.4%; Pred. No. 1.5e-67;
Matches 159; Conservative 21; Mismatches 12; Indels 1; Gaps 1;

QY 1 MFLVDMFYGFLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQYPTSEELS 60
DB 1 MFLVDMFYGFLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVQHOPQYPTSEELS 60

QY 61 INRVKFAFDLGGHTTARRVWRDYAKVDALVYLVDAVDRERFESKKEIDSLSDSL 120
DB 61 IGRKIKFAFDLGGHQAIRRVWRDYAKVDVAVYLVDAVDRERFESKKEIDSLSDSL 120

QY 121 QVPLVLTGNKIDIPYASSEDELRFTLGLT-MTTGKGVNLGDSNIRPIEVFMCISYVRKM 179
DB 121 TVPLIIGNKIDIPYASSEDELRVHLGLTGVTTGKGNINLAGTVVRPIEVFMCISYVRKM 180

QY 180 YGEGFKMVSQYIK 192
DB 181 YGEGFKMVSQYIK 193

RESULT 5
S28603
GTP-binding protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S28603
R:d'Entfert, C.; Genesee, M.; Galliard, C.
EMBO J. 11, 4205-4211, 1992
A:Title: Fission yeast and a plant have functional homologues of the Sar1 and Sec12 prote
A:Reference number: S28603; NID:93011016; PMID:1396601
A:Accession: S28603
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-193 <ENF>
A:Cross-references: UNIPROT:Q01474; UNIPARC:UPI0000001400; GB:M95795; NID:g166733; PIDN:
C:Superfamily: ADP-riboseylation factor
C:Keywords: GTP binding; nucleotide binding; P-loop
F:27-34/Region: nucleotide-binding motif A (P-loop)
F:129-132/Region: GTP-binding NKXD motif

Query Match 85.2%; Score 850.5; DB 2; Length 193;
Best Local Similarity 82.3%; Pred. No. 3.4e-67;
Matches 158; Conservative 20; Mismatches 13; Indels 1; Gaps 1;

QY 1 MFLVDMFYGFLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQYPTSEELS 60
DB 1 MFLVDMFYGFLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVQHOPQYPTSEELS 60

QY 61 INRVKFAFDLGGHTTARRVWRDYAKVDALVYLVDAVDRERFESKKEIDSLSDSL 120
DB 61 IGRKIKFAFDLGGHQAIRRVWRDYAKVDVAVYLVDAVDRERFESKKEIDSLSDSL 120

Db 61 IGIKFKAFDLSGHOIARRVWKDYAKVDVAVVLDVADYKERPAESKKEIDALLSDSEALA 120
QY 121 QVPLVVLGNKIDIPYASSEDELFTTGLT-MTTGKGVNLGDSNIRPIEVFMCISYVRKMG 179
Db 121 TVPFLITGNKIDIPYASSEDELRYHGLTNPFTTGKGVNLGDSGVRLPDEVFMCISYVRKMG 180
QY 180 YGEGFKMTQYI 191
Db 181 YGEGFKMTQYI 192

RESULT 6
small GTP-binding protein Bearia [imported] - turnip

C/Species: Brassica rapa (turnip)
C/Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C/Accession: T52094
R/Kim, W.Y.; Cheong, N.E.; Je, D.Y.; Kim, M.G.; Lim, C.O.; Bahk, J.D.; Cho, M.J.; Lee, S.
Plant Mol. Biol. 33, 1025-1035, 1997
A/Title: The presence of a Sar1 gene family in Brassica campestris that suppresses a yeast
A/Reference number: Z07935
A/Accession: T52094
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-193 <KIM>
A/Cross-references: UNIPROT:O04266; UNIPARC:UPI0000135566; EMBL:U55035; PIDD:AA049716.1
C/Genetics:
A/Genes: Bearia
C/Superfamily: ADP-ribosylation factor

Query Match 85.0%; Score 848.5; DB 2; Length 193;
Best Local Similarity 81.9%; Pred. No. 5,1e-67;
Matches 158; Conservative 22; Mismatches 12; Indels 1; Gaps 1;

QY 1 MFLVDFYFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSEELS 60
Db 1 MFLVDFYFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSEELS 60
QY 61 INRVKFAFDLGGHTIARRVWRDYAKVDVAVVLDVADYKERPAESKKEIDALLSDSELS 120
Db 61 IGIKFKAFDLSGHOIARRVWKDYAKVDVAVVLDVADYKERPAESKKEIDALLSDSELS 120
QY 121 QVPLVVLGNKIDIPYASSEDELFTTGLT-MTTGKGVNLGDSNIRPIEVFMCISYVRKMG 179
Db 121 TVPFLITGNKIDIPYASSEDELRYHGLTNPFTTGKGVNLGDSGVRLPDEVFMCISYVRKMG 180
QY 180 YGEGFKMTQYI 192
Db 181 YGEGFKMTQYI 193

RESULT 7

T52095 ras-like small monomeric GTP-binding protein [imported] - wild oat

C/Species: Avena fatua (wild oat)
C/Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C/Accession: T52095
R/Cranston, H.J.; Johnson, R.R.; Chaverra, M.E.; Dyer, W.E.
Plant Sci. 145, 75-81, 1999
A/Title: Isolation and characterization of a cDNA encoding a sar-like monomeric GTP-bind
A/Reference number: Z25949
A/Accession: T52095
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-193 <CRA>
A/Cross-references: UNIPROT:O81695; UNIPARC:UPI000009EBA3; EMBL:AF084005; PIDD:AA032610.
A/Experimental source: cultivar ANZ65
C/Genetics:
A/Genes: SARI
C/Superfamily: ADP-ribosylation factor

Query Match 84.5%; Score 843.5; DB 2; Length 193;
Best Local Similarity 81.8%; Pred. No. 1.4e-66;

Matches 157; Conservative 22; Mismatches 12; Indels 1; Gaps 1;

QY 1 MFLVDFYFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSEELS 60
Db 1 MFLVDFYFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSEELS 60
QY 61 INRVKFAFDLGGHTIARRVWRDYAKVDVAVVLDVADYKERPAESKKEIDALLSDSELS 120
Db 61 IGIKFKAFDLSGHOIARRVWKDYAKVDVAVVLDVADYKERPAESKKEIDALLSDSELS 120
QY 121 QVPLVVLGNKIDIPYASSEDELFTTGLT-MTTGKGVNLGDSNIRPIEVFMCISYVRKMG 179
Db 121 TVPFLITGNKIDIPYASSEDELRYHGLTNPFTTGKGVNLGDSGVRLPDEVFMCISYVRKMG 180
QY 180 YGEGFKMTQYI 191
Db 181 YGEGFKMTQYI 192

RESULT 8

T16993 GTP-binding protein Sar1, pollination-induced - apple tree

C/Species: Malus domestica (apple tree)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T16993
R/Dong, Y.H.; Kvarnheden, A.; Yao, J.L.; Sutherland, P.; Atkinson, R.; Morris, B.; Gardne
submitted to the EMBL Data Library, February 1998
A/Description: Identification of pollination-induced genes from the ovary of apple.
A/Reference number: Z18639
A/Accession: T16993
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-193 <DON>
A/Cross-references: UNIPROT:O65007; UNIPARC:UPI00000AC93D; EMBL:AF048825; NID:g2935451; I
A/Experimental source: cv. Granny Smith; fruit
C/Superfamily: ADP-ribosylation factor
C/Keywords: GTP binding; nucleotide binding; P-loop
P;27-34/Region: nucleotide-binding motif A (P-loop)
F;129-132/Region: GTP-binding NKXD motif

Query Match 83.7%; Score 835.5; DB 2; Length 193;
Best Local Similarity 81.9%; Pred. No. 7e-66;
Matches 158; Conservative 18; Mismatches 16; Indels 1; Gaps 1;

QY 1 MFLVDFYFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSEELS 60
Db 1 MFLVDFYFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSEELS 60
QY 61 INRVKFAFDLGGHTIARRVWRDYAKVDVAVVLDVADYKERPAESKKEIDALLSDSELS 120
Db 61 IGIKFKAFDLSGHOIARRVWKDYAKVDVAVVLDVADYKERPAESKKEIDALLSDSELS 120
QY 121 QVPLVVLGNKIDIPYASSEDELFTTGLT-MTTGKGVNLGDSNIRPIEVFMCISYVRKMG 179
Db 121 AVPLVVLGNKIDIPYASSEELRFHGLNFTTGKGVNLGDSNVRLPDEVFMCISYVRKMG 180
QY 180 YGEGFKMTQYI 192
Db 181 YGEGFKMTQYI 193

RESULT 9

T16966 GTP-binding protein (clone Np50SAR) - curled-leaved tobacco

C/Species: Nicotiana glauca (curled-leaved tobacco)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T16966
R/Borisejuk, N.
submitted to the EMBL Data Library, September 1996
A/Reference number: Z18620
A/Accession: T16966
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA

A;Residues: 1-194 <BOR>
A;Cross-references: UNIPROT:O24113; UNIPARC:UPI00000A178F; EMBL:Y08424
C;Superfamily: ADP-ribosylation factor
C;Keywords: GTP binding; nucleotide binding; P-loop
P;27-34/Region: nucleotide-binding motif A (P-loop)
F;129-132/Region: GTP-binding NKXD motif

Query Match 83.4%; Score 832; DB 2; Length 194;
Best Local Similarity 80.9%; Pred. No. 1.4e-65;
Matches 157; Conservative 22; Mismatches 13; Indels 2; Gaps 2;

QY 1 MFLVDMFYGLASIGLMQKAKILFLGLDNAGKTTLLHMLKDEKLGQHOPTPTSEELS 60
DB 1 MFLVDMFYGLASIGLMQKAKILFLGLDNAGKTTLLHMLKDEKLVQHQPPTPTSEELS 60
QY 61 INRVKFAFDLGGHTIARRVWDYAKVDVLYVDVADVRERPAESKKEKLDLSDLS 120
DB 61 IGRKIFKFAFDLGGHTIARRVWDYAKVDVLYVDVADVRERPAESKKEKLDLSDLSLA 120
QY 121 QVPVLVGNKIDIPYASSEDELRFITGLT-MTTGKGTVNLGDSNIRPIEFVFCISIVRMG 179
DB 121 TVPFLIIGNKIDIPYASSEDELRFYOMGLTITGKGVNLAEISVVRPLEVFCISIVRMG 180
QY 180 -YGEGRKMTQYIK 192
DB 181 IMAGFKMVSQYIK 194

RESULT 10

D86224
hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: D86224
R;Theologis, A.; Becker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, H.; Lin, Y.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maltli, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D86224
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-193 <STO>
A;Cross-references: UNIPROT:O80489; UNIPARC:UPI000009E5A2; GB:A8005172; NID:G3249104; P;
C;Genetics:
A;Map position: 1
C;Superfamily: ADP-ribosylation factor

Query Match 82.4%; Score 822.5; DB 2; Length 193;
Best Local Similarity 80.3%; Pred. No. 9.6e-65;
Matches 155; Conservative 20; Mismatches 17; Indels 1; Gaps 1;

QY 1 MFLVDMFYGLASIGLMQKAKILFLGLDNAGKTTLLHMLKDEKLGQHOPTPTSEELS 60
DB 1 MFLVDMFYGLASIGLMQKAKILFLGLDNAGKTTLLHMLKDEKLVQHQPPTPTSEELS 60
QY 61 INRVKFAFDLGGHTIARRVWDYAKVDVLYVDVADVRERPAESKKEKLDLSDLS 120
DB 61 IGRKIFKFAFDLGGHTIARRVWDYAKVDVLYVDVADVRERPAESKKEKLDLSDLSLA 120
QY 121 QVPVLVGNKIDIPYASSEDELRFITGLT-MTTGKGTVNLGDSNIRPIEFVFCISIVRMG 179
DB 121 NVPCIIIGNKIDIPYASSEDELRFYGLTNTFTTGKGVNLDSGVVRPLEVFCISIVRMG 180
QY 180 YGEGRKMTQYIK 192
DB 181 YGEGRKMTQYIK 193

RESULT 11

T03696
GTP-binding protein SAR1 - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03696
R;Shen, W.H.; Glog, C.
submitted to the EMBL Data Library, May 1996
A;Description: GTP-binding protein SAR1 of Nicotiana tabacum.
A;Reference number: Z15020
A;Accession: T03696
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-198 <SHE>
A;Cross-references: UNIPROT:P52865; UNIPARC:UPI0000135562; EMBL:X97967; NID:G1340114
A;Experimental source: strain Bright Yellow 2
C;Genetics:
A;Gene: SAR1
C;Superfamily: ADP-ribosylation factor
C;Keywords: GTP binding; nucleotide binding; P-loop
F;27-34/Region: nucleotide-binding motif A (P-loop)

Query Match 70.7%; Score 706; DB 2; Length 198;
Best Local Similarity 70.2%; Pred. No. 1.6e-54;
Matches 139; Conservative 22; Mismatches 31; Indels 6; Gaps 3;

QY 1 MFLVDMFYGLASIGLMQKAKILFLGLDNAGKTTLLHMLKDEKLGQHOPTPTSEELS 60
DB 1 MFLVDMFYGLATLGLMQKAKILFLGLDNAGKTTLLHMLKDEKLVQHQPPTPTSEELS 60
QY 61 INRVKFAFDLGGHTIARRVWDYAKVDVLYVDVADVRERPAESKKEKLDLSDLS 120
DB 61 IGRKIFKFAFDLGGHTIARRVWDYAKVDVLYVDVADVRERPAESKKEKLDLSDLS 120
QY 121 QVPVLVGN--KIDIPYAS-SEDELRFITGLTMT--GKGVNLGDSNIRPIEFVFCIS 174
DB 121 AHCFLEFLDMNVVITIEHICCLCRKQNRVHGANGASPLARKVNLDSNVRPVEVFCIS 180
QY 175 VRRKGVGEGRKMTQYIK 192
DB 181 VRRKGVGEGRKMTQYIK 198

RESULT 12

S28605
GTP-binding protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S28605; T40209
R;d'Enfert, C.; Gense, M.; Galliard, C.
EMBO J. 11, 4205-4211, 1992
A;Title: Fission yeast and a plant have functional homologues of the Sar1 and Sec12 prote

A;Reference number: S28605; MUID:93011016; PMID:11396601
A;Accession: S28605
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-190 <ENF>
A;Cross-references: UNIPROT:Q01475; UNIPARC:UPI0000135561; GB:M5797; NID:G173397; PIDN;
R;Wood, V.; Rajandream, M.A.; Barrett, B.G.; Pohl, T.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z21913
A;Accession: T40209
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-190 <WOO>
A;Cross-references: UNIPARC:UPI0000135561; EMBL:Z97204; PIDN:CAB10083.1; GSPDB:GN00067; E;
A;Experimental source: strain 972h-; cosmid c31f10
C;Genetics:
A;Gene: SPB31F10.06C
A;Map position: 2
A;Intons: 41/3; 77/1

QY 2 FLVDYMFY-GF---LASIGIMQKEAKILFELGLNAGNTTLLHMKDKELGQCHQCTOYPTSE 57
Db 3 FLEFIYNGFSSVLFGLGKYKSGKLVFLGLNAGNTTLLHMKDKDRLGQHVPTLLHPTSE 62
QY 58 ELISIRVYKPAVDLGSHITARRVWRDVAKVAIVLVAVDREPERAESKEXELDLSLD 11.7
Db 63 EULINGMTFTTDDLGSHEDQARRVYKNIYLPAINGIYVLVDCAHRSRLMESKVELNALMTDE 12.22
QY 118 SLQSPVPLVGNKKIDIPYASSEDELRFYIGL-TMTTGKTVNAGDSNIRPIEFVFGMSIVR 17.6
Db 123 TISNPIILLGNKIDRTDIAISEKKREITGLVGQTTGKNQVTLTKELNARMEVFMSVCK 10.2

Oy 177 KMGYGGGFKMTOYI 191
: |||||: ||||
Db 183 RGGYGGGFRWLSQYI 197

Search completed: December 9, 2005, 01:38:41
Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 01:10:11 ; Search time 158 seconds
(without alignments)
857.351 Million cell updates/sec

Title: US-10-688-481-11

Perfect score: 998

Sequence: 1 MFLVDMFYGRLASIGLWQKE.....SIVRKNMGYGRGFKMTQYIK 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	876.5	87.8	193	06PLR8_MAIZE	06plr8 zea mays (m
2	872.5	87.3	193	09SD05_TOBAC	09sd05 nicotiana t
3	871.5	86.5	193	SAR2_LYCES	P2884 lycopersico
4	863.5	86.4	193	SAR1A_ARATH	004834 arabidopsis
5	862.5	85.6	193	024110_NICPL	024110 nicotiana p
6	854.5	85.5	193	08VY07_ARATH	08vy07 arabidopsis
7	853.5	85.4	193	093W16_ORYSA	093w16 oryza sativ
8	852.5	85.2	193	SAR1B_ARATH	001474 arabidopsis
9	850.5	85.0	193	SAR1A_BRACM	004266 brassica ca
10	848.5	84.9	193	024138_TOBAC	024138 nicotiana t
11	847.5	84.5	193	081695_AVEFA	081695 avena fatua
12	843.5	84.5	193	065007_MALDO	065007 malus domes
13	835.5	83.7	193	024113_NICPL	024113 nicotiana p
14	832	83.4	194	SAR1B_BRACM	004266 brassica ca
15	831.5	82.4	193	080489_ARATH	080489 arabidopsis
16	822.5	82.4	193	067U02_ORYSA	067u02 oryza sativ
17	776.5	77.8	194	061V01_ORYSA	061v01 oryza sativ
18	758	76.0	193	SAR1_TOBAC	P58885 nicotiana t
19	706	70.7	198	09VD29_DROME	09vd29 drosophila
20	674.5	67.6	193	07P019_ANOGA	07p019 anopheles g
21	657.5	65.9	193	05KM05_CRYNE	05km05 cryplococcu
22	657	65.8	189	055XY7_CRYNE	055xy7 cryplococcu
23	657	65.6	191	08H713_PHYIN	08h713 phytophor
24	655	64.5	189	04P017_USTMA	04p017 ustialago ma
25	644	64.3	190	06CB54_YARLI	06cb54 yarrowia li
26	641.5	64.3	190	05XU06_9HEMI	05xu06 xanthopora c
27	635	63.6	192	SAR1_SCHPO	001475 aspergillus
28	628.5	63.0	190	04WJ57_ASPPU	04wj57 aspergillus
29	627	62.8	189	041812_GIBZE	041812 gibberella
30	627	62.8	189	0559R0_DICDI	0559r0 dictyosteli
31	625.5	62.7	188	0559R0_DICDI	0559r0 dictyosteli

32	625	62.6	140	040463_TOBAC	040463 nicotiana t
33	625	62.6	189	0877B9_ASPPU	0877b9 aspergillus
34	623	62.4	189	SAR1_TRIRE	P78976 trichoderma
35	622.5	62.4	211	05CVH4_CRYPV	05cvh4 crypsospori
36	621.5	62.3	197	09NFB8_DROME	09nfb8 drosophila
37	621.5	62.3	198	0567Y5_BRARE	0567y5 brachydanio
38	621	62.2	189	05BGB9_EMENT	05bgb9 aspergillus
39	620.5	62.2	193	05CKN9_CRYHO	05ckn9 crypsospori
40	619.5	62.1	190	SAR1_PICPA	09p48 pichia past
41	619	62.0	189	05EMZ6_MAGCR	05emz6 magnaporthe
42	619	62.0	189	052BE4_MAGCR	052be4 magnaporthe
43	616.5	61.7	198	SAR1B_MOUSE	09cgs mus muscula
44	615.5	61.7	198	04ZJK0_PIG	04zjk0 sus scrofa
45	614.5	61.6	198	SAR1B_CRIGR	09qvy3 cricetus

ALIGNMENTS

RESULT 1

ID	06PLR8_MAIZE	PRELIMINARY;	PRT;	193 AA.
AC	06PLR8;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	Putative ras-like small GTP binding protein.			
OS	Zea mays (Maize).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	PACCAD clade; Panicoideae; Andropogoneae; Zea.			
OX	NCBI_TaxID=4577;			
RN	[1]			
RP	NOCLBOTIDE SEQUENCE.			
RA	Zhang Z., Tang W., Zheng Y.;			
RL	Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.			
RU	EMBL: AY596178; AAT06576.1; -; mRNA.			
DR	GO: GO:0005794; C:Golgi apparatus; IEA.			
DR	GO: GO:0005525; F:GTP binding; IEA.			
DR	GO: GO:0006886; F:intracellular protein transport; IEA.			
DR	GO: GO:0007264; P:small GTPase mediated signal transduction; IEA.			
DR	InterPro: IPR006688; ARF.			
DR	InterPro: IPR006689; ARF/SAR.			
DR	InterPro: IPR001806; Ras trnsfmrng.			
DR	InterPro: IPR006687; SAR1.			
DR	InterPro: IPR005225; Small_GTP.			
DR	Pfam: PF00025; Arf; 1.			
DR	PRINTS: PR00449; RASTRNSFRMG.			
DR	PRINTS: PR00328; SAR1GTPBP.			
DR	SMART: SM00177; ARF; 1.			
DR	SMART: SM00178; SAR; 1.			
DR	TIGRFAMs: TIGR00231; small_GTP; 1.			
DR	TIGRFAMs: TIGR00231; small_GTP; 1.			
DR	SEQUENCE 193 AA; 22012 MW; EF9167BD74E2DF68 CRC64;			

Query Match 87.8%; Score 876.5; DB 2; Length 193;

Best Local Similarity 83.9%; Pred. No. 7e-65; Mismatches 10; Indels 1; Gaps 1;

Matches 162; Conservative 20; Mismatches 10; Indels 1; Gaps 1;

QY	1	MFLVDMFYGRLASIGLWQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHPTQPTSELS	60
DB	1	MFLVDMFYGRLASIGLWQKEAKILFLGLDNAGKTTLLHMLKDEKLVQHPTQPTSELS	60
QY	61	INRYKFAFPLGGHTTIRRWRYAVDAIVYLVDAVDREPRPESKKEIDSLSDSLS	120
DB	61	IGRIKFAFPLGGHTTIRRWRYAVDAIVYLVDAVDREPRPESKKEIDSLSDSLS	120
QY	121	QVPLVYGNKIDIPYASSEDLRPTLGLT-MTGGKGTVNLGDSNIRPIEVFMCISVRMG	179
DB	121	NVPLILGNKIDIPYASSEDLRPTLGLT-MTGGKGTVNLGDSNIRPIEVFMCISVRMG	180
QY	180	YGBGFKMTQYIK 192	
DB	181	YGBGFKMTQYIK 193	


```

RESULT 2
Q9SDK4_ORYSA PRELIMINARY; PRT; 193 AA.
ID Q9SDK4_ORYSA
AC Q9SDK4_
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Putative small GTP-binding protein Baaria (GTP-binding protein).
GN Name=PO705D01.9; Synonyms=GBP;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsunoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Maekawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Higashita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikeno M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
RA Katsawa W., Katagiri S., Kikuta A., Kodayashi N., Kono I.,
RA Mochida K., Maehara T., Mizuno H., Mizuyasahi Y., Mukai Y.,
RA Nagasaka K., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhang H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RA Meng X.-B., Lin R.-W., Wang M., Zhao W.-S., Peng Y.-L.;
RL Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.
CC -1 SIMILARITY: Belongs to the small GTPase superfamily.
DR EMBL; AP000492; BA84612.1; -; Genomic_DNA.
DR EMBL; AY620417; AAT28677.1; -; mRNA.
DR HSSP; O9OYV3; 1F6B.
DR Gtname; Q9SDK4; -.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0006886; P:intracellular protein transport; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR006689; ARF/SAR.
DR InterPro; IPR001806; Ras_trnsfrmg.
DR InterPro; IPR006687; SAR1_GTP_bd.
DR InterPro; IPR005225; Small_GTP_bd.
DR Pfam; PF00025; Arf; 1.
DR PRINTS; PR00449; RASTRSPFRMG.
DR PRINTS; PR00328; SAR1GTPBP.
DR SMART; SM00178; SAR; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR GTP-binding; Nucleotide-binding.
DR GTP-binding; Nucleotide-binding.
SQ SEQUENCE 193 AA; 21944 MW; BCAC934283DEC7E CRC64;

Query Match 87.4%; Score 872.5; DB 2; Length 193;
Best Local Similarity 83.4%; Pred. No. 1.5e-64;
Matches 161; Conservative 20; Mismatches 11; Indels 1; Gaps 1;

QY 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGHOPTQYPTSEELS 60
DB 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGHOPTQYPTSEELS 60
QY 61 INRYKFAFDLGGTTIARRWRDYYAKVDALVYLVDADVDRERFAESKKEIDSLSDSLS 120
DB 61 IGIKIKFAFDLGGTTIARRWRDYYAKVDALVYLVDADVDRERFAESKKEIDSLSDSLS 120
QY 121 QVPLVVGNNKIDIPYASSEDRLRFTLGIT-MTTGKGTVNLGDSNIRPIEFVMCSIVRMKG 179
DB 121 TVPFLILGNKIDIPYASSEDRLRFTLGIT-MTTGKGTVNLGDSNIRPIEFVMCSIVRMKG 179
QY 121 TVPFLILGNKIDIPYASSEDRLRFTLGIT-MTTGKGTVNLGDSNIRPIEFVMCSIVRMKG 180
DB 121 TVPFLILGNKIDIPYASSEDRLRFTLGIT-MTTGKGTVNLGDSNIRPIEFVMCSIVRMKG 180

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QY 180 YGEGFKMNTQYIK 192
DB 181 YGEGFKMNSQYIK 193

RESULT 3
Q9SD05_TOBAC PRELIMINARY; PRT; 193 AA.
ID Q9SD05_TOBAC
AC Q9SD05_
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Small GTP-binding protein Sar1BNC.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tissue= Mature leaves;
RA Andreeva A.V., Kutuzov M.A., Evans D.E., Hawes C.R.;
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
CC -1 SIMILARITY: Belongs to the small GTPase superfamily.
DR EMBL; AF210431; AAF17254.1; -; mRNA.
DR PIR; T52096; T52096.
DR HSSP; O9OYV3; 1F6B.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0006886; P:intracellular protein transport; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR006689; ARF/SAR.
DR InterPro; IPR001806; Ras_trnsfrmg.
DR InterPro; IPR006687; SAR1_GTP_bd.
DR InterPro; IPR005225; Small_GTP_bd.
DR Pfam; PF00025; Arf; 1.
DR PRINTS; PR00449; RASTRSPFRMG.
DR PRINTS; PR00328; SAR1GTPBP.
DR SMART; SM00178; SAR; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR PROSITE; PS01020; SAR1; 1.
DR GTP-binding; Nucleotide-binding.
SQ SEQUENCE 193 AA; 22010 MW; 118CF5894EB6BF4E CRC64;

Query Match 87.3%; Score 871.5; DB 2; Length 193;
Best Local Similarity 83.4%; Pred. No. 1.8e-64;
Matches 161; Conservative 21; Mismatches 10; Indels 1; Gaps 1;

QY 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGHOPTQYPTSEELS 60
DB 1 MFLVDMFYGLATLIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGHOPTQYPTSEELS 60
QY 61 INRYKFAFDLGGTTIARRWRDYYAKVDALVYLVDADVDRERFAESKKEIDSLSDSLS 120
DB 61 IGIKIKFAFDLGGTTIARRWRDYYAKVDALVYVDSFDERFAESKKEIDSLSDSLSLA 120
QY 121 QVPLVVGNNKIDIPYASSEDRLRFTLGIT-MTTGKGTVNLGDSNIRPIEFVMCSIVRMKG 179
DB 121 TVPFLILGNKIDIPYASSEDRLRFTLGIT-MTTGKGTVNLGDSNIRPIEFVMCSIVRMKG 180
QY 180 YGEGFKMNTQYIK 192
DB 181 YGEGFKMNSQYIK 193

RESULT 4
ID SAR2_LYCES STANDARD; PRT; 193 AA.
AC P52884;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE GTP-binding protein SAR2.

```


GN Name=SAR2;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Asterids; Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
OX NCBI_TaxID=4081;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pericarp;
RX MEDLINE=94169306; PubMed=8123794;
RA Davies C.;
RT "Cloning and characterization of a tomato GTPase-like gene related to
the yeast Arabidopsis genes involved in vesicular transport.";
RL Plant Mol. Biol. 24:525-531(1994).
CC - FUNCTION: Involved in transport from the endoplasmic reticulum to
the Golgi apparatus (by similarity).
CC - SIMILARITY: Belongs to the small GTPase superfamily, SAR1 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC EMBL: L12051; AAA34168.1; -; mRNA.
DR PIR: S42528; S42528.
DR HSSP: Q9QVY3; 1P6B.
DR InterPro: IPR006689; ARF/SAR.
DR InterPro: IPR001806; Ras_trnsmfrmg.
DR InterPro: IPR006687; SAR1_GTP_bd.
DR InterPro: IPR005225; Small_GTP_bd.
DR PANTHER: PTHR11711; ARF/SAR; 1.
DR Pfam: PF000025; Arf; 1.
DR PRINTS: PR00449; RASTRNSFRMG.
DR PRINTS: PR00328; SAR1GTPBP.
DR SMART: SM00178; SAR; 1.
DR TIGRFAMs: TIGR00231; small_GTP; 1.
DR PROSITE: PS01020; SAR1; 1.
KM Endoplasmic reticulum; ER-Golgi transport; Golgi stack; GTP-binding;
KW Nucleotide-binding; Protein transport; Transport.
FT NP_BIND 27 GTP (By similarity).
FT NP_BIND 70 GTP (By similarity).
FT NP_BIND 129 132 GTP (By similarity).
SQ SEQUENCE 193 AA; 21923 MW; CF5223DB9D599BAF CRC64;
Query Match 86.5%; Score 863.5; DB 1; Length 193;
Best Local Similarity 83.9%; Pred. No. 8.5e-64;
Matches 162; Conservative 16; Mismatches 14; Indels 1; Gaps 1;
QY 1 MFLVDFPYGLASIGLMOKAKILFLGLDNAGKTTLLHMLKDEKLGQHPTQYPTSELS 60
DB 1 MFLVDFPYGLASIGLMOKAKILFLGLDNAGKTTLLHMLKDEKLGQHPTQYPTSELS 60
QY 61 INNVKFAKAPLGGHTTARVWRDYAKVDIVYLVDAVDREPERAESKEDSLSDSL 120
DB 61 INNVKFAKAPLGGHTTARVWRDYAKVDIVYLVDAVDREPERAESKEDSLSDSL 120
QY 61 IGNIKKRKPGLGGHQLARKRWRYAKVDIVYLVDAVDREPERAESKEDSLSDSL 120
DB 61 IGNIKKRKPGLGGHQLARKRWRYAKVDIVYLVDAVDREPERAESKEDSLSDSL 120
QY 121 QVEVLVGNKIIDIPYASSEDELRFTGLT-MTTGKGTVNLGDSNIRPIEIVFMCISYKMG 179
DB 121 NVPFLLIGNKIIDIPYASSEDELRHGLTGVTTGKGNINLGNVVRPIEIVFMCISYKMG 180
QY 180 YGEGFKMMTOYIK 192
DB 181 YGEGFKMMTOYIK 193

DE GTP-binding protein SAR1A.
GN Name=SAR1A; OrderedLocustNames=At4g02080; ORFNames=T10M13.9, AGAA.4;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosids; eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. Columbia;
RA Winge P., Brembu T., Bones A.M.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=cv. Columbia; PubMed=10617198; DOI=10.1038/47134;
RX MEDLINE=20083468; PubMed=10617198; DOI=10.1038/47134;
RA Mayer K.F.X., Scheller C., Wambutt R., Murphy G., Volkert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Ertter K.-D., Terry N.,
RA Harris B., Ansgore W., Brandt P., Griwell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermayer B., Maché R., Mueller M.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidheini T.,
RA Reichert B., Portetelie D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hohnel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schuren J., Grymoprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzengger T., Bothé G., Rasperger U., Hilbert H., Braun M.,
RA Holzner E., Brandt A., Peters S., van Staeren M., Dirke W.,
RA Woolfman P., Klein Lankhorst R., Rose M., Hauf J., Koelter P.,
RA Bernsieser S., Hempel S., Feldpausch M., Lambert S., Van den Daele H.,
RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIay K., Mayes R.,
RA Peetec A., Rajandream M.A., Lyne M., Benes V., Reckmann S.,
RA Borkova D., Bloeker H., Scharte M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Marase A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartman B., Granderach K., Dauner D., Herzi A.,
RA Neumann O., Angileu A., Vitale D., Liguori R., Piravadi B.,
RA Samsad S., Hiller R., Schmidt W., Lechary A., Aubourg S.,
RA Ghidoui F., Cooke R., Berger C., Montfort A., Caescheberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacou D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Frances P., Bielke C.,
RA Frisman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Baetle M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stronging T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Mink P., Bentley D., Fulton L., Mardis E., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joehu C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Sheker M., Macero A., Shah R.,
RA Saby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Grant S., Shohdy N., Hasegawa A., Hamed A., Lodi M., Johnson A.,
RA Chen E., Maria M.A., Martienssen R., McCormie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
thaliana.";
RL Nature 402:769-777(1999).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. Landsberg erecta;
RA Till S., Grant S., Parnell L., Kaplan N., Hoffman J., Lodi M.,
RA Johnson A.F., Dedhia N., Martienssen R., McCormie W.R.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=cv. Columbia; PubMed=14593172; DOI=10.1126/science.1086305;
RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1086305;
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,

RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
 RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
 RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
 RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
 RA Akawa T., Banh J., Banno F., Brooks S.Y., Carinci P.,
 RA Chao Q., Choy N., Enju A., Goldenrich A.D., Gurjal M., Hansen N.F.,
 RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
 RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
 RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
 RA Satou M., Tame R., Vaynsberg M., Wallender E.K., Wong C., Yamamura Y.,
 RA Yuan S., Shirozaki K., Davis R.W., Theologis A., Ecker J.R.,
 RT "Empirical analysis of transcriptional activity in the Arabidopsis
 RT genome.",
 RL Science 302:842-846(2003).
 RN [5]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RA Brover V., Trounhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.A.,
 RT "Full-length cDNA from Arabidopsis thaliana.",
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 104-193.
 RC STRAIN=cv. Columbia; TISSUE=seedling;
 RX MEDLINE=96159348; PubMed=8580968;
 RI DOI=10.1046/j.1365-3113.1996.09010101.x;
 RA Cooke R., Raynal M., Laudie M., Grellet F., Delzeny M., Morris P.-C.,
 RA Guerrier D., Giraudat J., Quigley F., Chabault G., Li Y.-F., Maché R.,
 RA Krivitzky M., Gy I.J.-J., Kreis M., Lecharny A., Parmentier Y.,
 RA Marbach J., Fleck J., Clement B., Philippe G., Hervé C., Bardet C.,
 RA Tremoussaygue D., Leasure B., Lacomme C., Roby D., Jourjon M.-F.,
 RA Chabrier P., Charpentier J.-L., Desprez T., Amselem J., Chappellet H.,
 RA Hoeft H.,
 RT "Further progress towards a catalogue of all Arabidopsis genes:
 RT analysis of a set of 5000 non-redundant ESTs.",
 RL Plant J. 9:101-124(1996).
 CC -1- FUNCTION: Involved in transport from the endoplasmic reticulum to
 CC the Golgi apparatus (By similarity).
 CC -1- SIMILARITY: Belongs to the small GTPase superfamily. SAR1 family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL: U56929; AAA93827.1; -; mRNA.
 DR EMBL: AF001308; AAC78700.1; -; Genomic DNA.
 DR EMBL: AL161493; CAB80701.1; -; Genomic DNA.
 DR EMBL: AF001535; AAB57799.1; -; Genomic DNA.
 DR EMBL: AY065357; AAL38798.1; -; mRNA.
 DR EMBL: AY096699; AAM20333.1; -; mRNA.
 DR EMBL: AY088765; AAM67080.1; -; mRNA.
 DR EMBL: Z26707; CAA81406.1; -; mRNA.
 DR PIR: T01509; T01509.
 DR HSSP: Q9QVY3; 1F6B.
 DR InterPro: IPR006689; ARF/SAR.
 DR InterPro: IPR001806; Ras trnsfmg.
 DR InterPro: IPR006687; SAR1 GTP bd.
 DR InterPro: IPR005225; Small GTP bd.
 DR PANTHER: PTHR11711; ARF/SAR; 1.
 DR Pfam: PF00025; Arf; 1.
 DR PRINTS: PR00449; RASTRNSFRMG.
 DR PRINTS: PR00328; SAR1GTPBP.
 DR SMART: SM00178; SAR; 1.
 DR TIGRfam: TIGR00231; small_GTP; 1.
 DR PROSITE: PS01020; SAR1; 1.
 KW Endoplasmic reticulum; ER-Golgi transport; Golgi stack; GTP-binding;
 KM Nucleotide-binding; Protein transport; Transport.
 FT NP_BIND 27 34 GTP (By similarity).
 FT NP_BIND 70 73 GTP (By similarity).
 FT NP_BIND 129 132 GTP (By similarity).
 SQ SEQUENCE 193 AA; 22030 MW; 641D1664548A0BE CRC64;

Query Match 86.4%; Score 862.5; DB 1; Length 193;
 Best Local Similarity 82.4%; Pred. No. 1e-63;
 Matches 160; Conservative 21; Mismatches 11; Indels 1; Gaps 1;
 QY 1 MFLVDFYFGFLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPFOYPTSELS 60
 DB 1 MFLVDFYFGFLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKRLVQHOPFOYPTSELS 60
 QY 61 INRKFRAPDLGGHTTARRVWRDYAKVDAIVYLVDVDERPAESKEKELSDLSDSLS 120
 DB 61 IGKIKFAFDLGGHQLARRVWKDYAKVDAVVYLVDVDERPAESKEKELDALLSDLSLA 120
 QY 121 QVPLVVLGNKIDIPYASSEDELRFITGLT-MTTGKGTVNLGDSNIRPIVFMCSIVKMG 179
 DB 121 SVPLILGNKIDIPYASSEDELRYHLGLSNFTTGKRVNLDSNVRLPVEVFMCSIVKMG 180
 QY 180 YGEFGFKMTQYIK 192
 DB 181 YGEFGFKMTQYIK 193
 RESULT 6
 ID 024110_NICPL PRELIMINARY; PRT; 193 AA.
 AC 024110;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JUN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Small GTP-binding protein.
 OS Nicotiana glauca (leadwort-leaved tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC asterids; lamiales; Solanales; Solanaceae; Nicotiana.
 OC NCBI_TaxID=4092;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Borisyuk N.,
 RT Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the small GTPase superfamily.
 DR EMBL: Y08423; CAA69699.1; -; mRNA.
 DR PIR: T16964; T16964.
 DR HSSP: Q9QVY3; 1F6B.
 DR GO: GO:0005525; F:GTP binding; IEA.
 DR GO: GO:0006886; P:intracellular protein transport; IEA.
 DR GO: GO:0007264; P:small GTPase mediated signal transduction; IEA.
 DR InterPro: IPR006689; ARF/SAR.
 DR InterPro: IPR001806; Ras trnsfmg.
 DR InterPro: IPR006687; SAR1 GTP bd.
 DR InterPro: IPR005225; Small GTP bd.
 DR Pfam: PF00025; Arf; 1.
 DR PRINTS: PR00449; RASTRNSFRMG.
 DR PRINTS: PR00328; SAR1GTPBP.
 DR SMART: SM00178; SAR; 1.
 DR TIGRfam: TIGR00231; small_GTP; 1.
 DR PROSITE: PS01020; SAR1; 1.
 KW GTP-binding; Nucleotide-binding.
 SQ SEQUENCE 193 AA; 21935 MW; F2718819740F506E CRC64;
 Query Match 85.6%; Score 854.5; DB 2; Length 193;
 Best Local Similarity 82.4%; Pred. No. 4.8e-63;
 Matches 159; Conservative 21; Mismatches 12; Indels 1; Gaps 1;
 QY 1 MFLVDFYFGFLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPFOYPTSELS 60
 DB 1 MFLVDFYFGFLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKRLVQHOPFOYPTSELS 60
 QY 61 INRKFRAPDLGGHTTARRVWRDYAKVDAIVYLVDVDERPAESKEKELSDLSDSLS 120
 DB 61 IGKIKFAFDLGGHQLARRVWKDYAKVDAVVYLVDVDERPAESKEKELDALLSDLSLA 120
 QY 121 QVPLVVLGNKIDIPYASSEDELRFITGLT-MTTGKGTVNLGDSNIRPIVFMCSIVKMG 179
 DB 121 TVPLILGNKIDIPYASSEDELRYHLGLTVTTGKRVNLDSNVRLPVEVFMCSIVKMG 180

QY 180 YGEGFKMTQYIK 192
 DB 181 YGEGFKMTQYIK 193

RESULT 7
 Q8VVP7 ARATH PRT; 193 AA.

AC Q8VVP7, 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Putative SARI GTP binding protein.
 GN Name=At3g62560;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie.
 NCBI_TaxID=3702;

RA NUCLEOTIDE SEQUENCE.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shinn P., Southwick A., Shinzaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

RP NUCLEOTIDE SEQUENCE.
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shinn P., Southwick A., Shinzaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the small GTPase superfamily.
 DR EMBL: AY070378; AAL49874.1; -; mRNA.
 DR EMBL: AY117363; AAMS1438.1; -; mRNA.
 DR HSSP: Q9GVY3; 1F6B.
 DR GO: GO:0005525; F:GTP binding; IEA.
 DR GO: GO:0006886; P:intracellular protein transport; IEA.
 DR GO: GO:0007264; P:small GTPase mediated signal transduction; IEA.
 DR InterPro: IPR006689; ARF/SAR.
 DR InterPro: IPR001806; Ras_trnfamg.
 DR InterPro: IPR006687; SARI_GTP_bd.
 DR InterPro: IPR005225; Small_GTP_bd.
 DR Pfam: PF00025; Arf; 1.
 DR PRINTS: PR00449; RASTRSPFMNG.
 DR PRINTS: PR00328; SARICGTPP.
 DR SMART: SM00178; SAR; 1.
 DR TIGRFAMs: TIGR00231; small_GTP; 1.
 DR PROSITE: PS01020; SARI; 1.
 KM GTP-binding; Nucleotide-binding.
 SQ SEQUENCE 193 AA; 21939 MW; AA7D50764B3F848 CRC64;

Query Match 85.5%; Score 853.5; DB 2; Length 193;
 Best Local Similarity 82.8%; Pred. No. 5.8e-63;
 Matches 159; Conservative 20; Mismatches 12; Indels 1; Gaps 1;

QY 1 MFLVDWYVYGLASIGLMQKAKILFLGLDNAGKTTLLHMLKDEKLGQHOPTQYPTSELS 60
 DB 1 MFLVDWYVYGLATIGLMQKAKILFLGLDNAGKTTLLHMLKDEKLVGHOPQHTSELS 60
 QY 61 INRVKFAFDLGGHTIARRVWDYVAKVDALVYLVDVDRERFAESKKEIDSLSDSLS 120
 DB 61 IGKIKFAFDLGGHQAARRVWKDYVAKVDVAVVYLVDVDRERFAESKKEIDSLSDSLS 120

QY 121 QVPLVILGNKIDIPVASEDELRFTGLT-MTTGKGTVNLGDSNIRPIEFVMSIYRKNG 179
 DB 121 NVPLILGNKIDIPVASEDELRFTGLTSGFTGKGVNLGAGTVNPLFVFMCSIVRKNG 180
 QY 180 YGEGFKMTQYI 191
 DB 181 YGEGFKMTQYI 192

RESULT 8
 Q93W16 ORYSA PRT; 193 AA.

AC Q93W16, 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Putative small GTP-binding protein Basarla.
 GN Name=B1088D01.1; Synonyms=P0487E11.37;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NCBI_TaxID=39447;

RA NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
 RA Wu J., Nishimura Y., Cheng Z., Nagamura Y., Antono B.A., Kanamori H.,
 RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
 RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
 RA Ikono M., Itoh S., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
 RA Karasawa M., Katsufiri S., Kikuta A., Kobayashi N., Kono I.,
 RA Machita K., Maehara T., Mizuno H., Mizuyashi T., Mukai Y.,
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Teuji K.,
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
 RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
 RA Yano M., Jiang J., Gojobori T.;
 RA "The genome sequence and structure of rice chromosome 1.";
 RL Nature 420:312-316(2002).
 CC -1- SIMILARITY: Belongs to the small GTPase superfamily.
 DR EMBL: AP003331; BAB6797.1; -; Genomic DNA.
 DR EMBL: AP003793; BAB63877.1; -; Genomic DNA.
 DR HSSP: Q9GVY3; 1F6B.
 DR Gramene: Q93W16; -.

DR GO: GO:0005525; F:GTP binding; IEA.
 DR GO: GO:0006886; P:intracellular protein transport; IEA.
 DR GO: GO:0007264; P:small GTPase mediated signal transduction; IEA.
 DR InterPro: IPR006689; ARF/SAR.
 DR InterPro: IPR001806; Ras_trnfamg.
 DR InterPro: IPR006687; SARI_GTP_bd.
 DR InterPro: IPR005225; Small_GTP_bd.
 DR Pfam: PF00025; Arf; 1.
 DR PRINTS: PR00449; RASTRSPFMNG.
 DR PRINTS: PR00328; SARICGTPP.
 DR SMART: SM00178; SAR; 1.
 DR TIGRFAMs: TIGR00231; small_GTP; 1.
 DR PROSITE: PS01020; SARI; 1.
 KM GTP-binding; Nucleotide-binding.
 SQ SEQUENCE 193 AA; 21984 MW; 65351FBI40BAD9 CRC64;

Query Match 85.4%; Score 852.5; DB 2; Length 193;
 Best Local Similarity 81.9%; Pred. No. 7e-63;
 Matches 158; Conservative 23; Mismatches 11; Indels 1; Gaps 1;

QY 1 MFLVDWYVYGLASIGLMQKAKILFLGLDNAGKTTLLHMLKDEKLGQHOPTQYPTSELS 60
 DB 1 MFLVDWYVYGLASIGLMQKAKILFLGLDNAGKTTLLHMLKDEKLVGHOPQHTSELS 60
 QY 61 INRVKFAFDLGGHTIARRVWDYVAKVDALVYLVDVDRERFAESKKEIDSLSDSLS 120
 DB 61 IGKIKFAFDLGGHQAARRVWKDYVAKVDVAVVYLVDVDRERFAESKKEIDSLSDSLS 120

QY 121 QVPVLVGNKIDIPYASSEDEBLRFTLGIT-MTGGKGVNIGDSNIRPIEVFMCIVAKMG 179
 DB 121 AVPELLIGNKKIDIPYASSEELRYHLGISTFTGKGVNIGDSNIRPIEVFMCIVAKMG 180
 QY 180 YGSGFKMTQYIK 192
 DB 181 YGSGFKMTQYIK 193

RESULT 9
 SARI.B ARATH STANDARD; PRT; 193 AA.
 ID SARI.B ARATH
 AC 001474;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE GTP-binding protein SARI.B.
 GN Name=SARI.B; Synonym=SARI; OrderedLocustNames=At1g56330;
 OR Names=Fl4g9.6;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosoid II; Brassicales; Brassicaceae; Arabidopses.
 OC NCBI TaxID=3702;
 RX MEDLINE=21016719; PubMed=1130712; DOI=10.1036/35048500;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
 Buhler E., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K.,
 Dunn P., Egtu P., Feldlyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 Kim C.J., Koo H.L., Kremetskaia I., Kurtz D.B., Kwan A., Lam B.,
 Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
 Miltseher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 Utecherback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RA "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana.";
 RL Nature 408:816-820(2000).
 RP STRAIN=cv. Columbia;
 RC MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
 RX Yamada K., Lim U., Dale J.M., Chen H., Shinn P., Palm C.J.,
 Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
 Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
 Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
 Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
 Arakawa T., Banh U., Banno F., Bowser L., Brooks S.Y., Carninci P.,
 Chao Q., Choy N., Ejub A., Goldsmith A.D., Guiral M., Hansen N.F.,
 Hayashizaki Y., Johnson-Hopson C., Hsu V.M., Iida K., Karnes M.,
 Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
 Kamuya A., Meyers C., Nakejima M., Narusaka M., Seki M., Sakurai T.,
 Satou M., Tame R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
 Yuan S., Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;
 RA "Empirical analysis of transcriptional activity in the Arabidopsis
 genome.";

RL Science 302:842-846(2003).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RA Brover V., Trukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.A.;
 RT "Full-length cDNA from Arabidopsis thaliana."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Involved in transport from the endoplasmic reticulum to
 CC the Golgi apparatus (By similarity).
 CC -1- SIMILARITY: Belongs to the small GTPase superfamily. SARI family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL nucleotide
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 DR EMBL: M95795; AAA32807.1; -; mRNA.
 DR EMBL: AC069159; AAG50911.1; -; Genomic DNA.
 DR EMBL: AY072220; AAL60041.1; -; mRNA.
 DR EMBL: AY096559; AAM20249.1; -; mRNA.
 DR EMBL: AY085815; AAM63031.1; -; mRNA.
 DR PIR: S28603; S28603.
 DR HSP: Q9QVY3; 1P68.
 DR InterPro: IPR006689; ARF/SAR.
 DR InterPro: IPR001806; Ras_trnsmfmg.
 DR InterPro: IPR006687; SARI_GTP_bd.
 DR InterPro: IPR005225; Small GTP bd.
 DR PANTHER: PTHR11711; ARF/SAR; 1.
 DR Pfam: PF00025; Arf; 1.
 DR PRINTS: PR00449; RASTRNSPRMNG.
 DR PRINTS: PR00328; SARIGTPBP.
 DR SMART: SM00178; SAR; 1.
 DR TIGRFAMs: TIGR00231; small_GTP; 1.
 DR PROSITE: PS01020; SARI; 1.
 DR KX Endoplasmic reticulum; ER-Golgi transport; Golgi stack; GTP-binding;
 KM Nucleotide-binding; Protein transport; Transport.
 FT NP_BIND 27 34 GTP (By similarity).
 FT NP_BIND 70 73 GTP (By similarity).
 FT NP_BIND 129 132 GTP (By similarity).
 SQ SEQUENCE 193 AA; 21986 MW; 9D9AE86B3BE68878 CRC64;
 QY Query Match 85.2%; Score 850.5; DB 1; Length 193;
 Best Local Similarity 82.3%; Pred. No. 1e-62;
 Matches 158; Conservative 20; Mismatches 13; Indels 1; Gaps 1;
 QY 1 MELVDWVYGLASIGLQKAKILFLGLDNAGKTTLLHMLKDEKLGQHOPTQYTSSELS 60
 DB 1 MFLFDWYFGILASIGLQKAKILFLGLDNAGKTTLLHMLKDEKLVQHOPTQYTSSELS 60
 QY 61 INRYKFAFPLDGGHTIARRVWDYAKVDAIVLVDAVDERPAESKKEKELSDLS 120
 DB 61 IGRKIFAFPLDGGHGIARRVWDYAKVDAIVLVDAVDERPAESKKEKELSDLS 120
 QY 121 QVPVLVGNKIDIPYASSEDEBLRFTLGIT-MTGGKGVNIGDSNIRPIEVFMCIVAKMG 179
 DB 121 TVPFLIGNKKIDIPYASSEELRYHLGISTFTGKGVNIGDSNIRPIEVFMCIVAKMG 180
 QY 180 YGSGFKMTQYIK 191
 DB 181 YGSGFKMTQYIK 192

RESULT 10
 SARI.B BRACM STANDARD; PRT; 193 AA.
 ID SARI.B BRACM
 AC 004266;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE GTP-binding protein SARI.B.
 GN Name=SARI.B;
 OS Brassica campestris (field mustard).
 OS

CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 CC rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 CC NCBI_TaxID=3711;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=97298835; PubMed=9154984; DOI=10.1023/A:1005733209124;
 RA Kim W.Y., Cheong N.E., Je D.Y., Kim M.G., Lim C.O., Bahk J.D.,
 RA Cho M.J., Lee S.Y.;
 RT "The presence of a SARI gene family in *Brassica campestris* that
 RT suppresses a yeast vesicular transport mutation Sec12-1.";
 RL Plant Mol. Biol. 33:1025-1035(1997).
 CC -1- FUNCTION: Involved in transport from the endoplasmic reticulum to
 CC the Golgi apparatus (By similarity).
 CC -1- TISSUE SPECIFICITY: Expressed in most tissues.
 CC -1- SIMILARITY: Belongs to the small GTPase superfamily. SARI family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: U55035; AAC49716.1; -; mRNA.
 DR PIR: T52094; T52094.
 DR HSSP: Q9QVY3; 1F6B.
 DR InterPro: IPR006689; ARF/SAR.
 DR InterPro: IPR001806; Ras_crnsmfng.
 DR InterPro: IPR006687; SARI_GTP_bd.
 DR InterPro: IPR005225; Small_GTP_bd.
 DR PANTHER: PTHR11711; ARF/SAR; 1.
 DR Pfam: PF00025; Arf; 1.
 DR PRINTS: PR00449; RASTNSFRMG.
 DR PRINTS: PR00328; SARI_GTPBP.
 DR SMART: SM00178; SAR; 1.
 DR TIGRFAMs: TIGR00231; small_GTP; 1.
 DR PROSITE: PS01020; SARI; 1.
 KM Endoplasmic reticulum: ER-Golgi transport; Golgi stack; GTP-binding;
 KM Nucleotide-binding; Protein transport; Transport.
 FT NP BIND 27 34 GTP (By similarity).
 FT NP BIND 70 73 GTP (By similarity).
 FT NP BIND 129 132 GTP (By similarity).
 SQ SEQUENCE 193 AA; 21967 MW; 454398FF39721F66 CRC64;
 Query Match 85.0%; Score 848.5; DB 1; Length 193;
 Best Local Similarity 81.9%; Pred. No. 1.5e-62;
 Matches 158; Conservative 22; Mismatches 12; Indels 1; Gaps 1;
 QY 1 MFLVDMFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHPOTQPTSEELS 60
 DB 1 MFLVDMFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHPOTQPTSEELS 60
 QY 61 INRVKFAFDLGGHTTARVWDYAKVDAIVLVDAVDEREFAESKKELDLSLSDSL 120
 DB 61 IGRKIFKAFDGLGQIARVWKDYAKVDAIVLVDAVDEREFAESKKELDLSLSDSLA 120
 QY 121 QVPLVLGNKIDIPYASSEDELRLFTGLT-MTTGKGTVNLGDSNIRPIEVFMCSIVRKMG 179
 DB 121 TVPFLILGNKIDIPYASSEDELRLHGLISNFTTGKGVLDVGSVNRPLEVFMCSIVRKMG 180
 QY 180 YGEGFKMNTQYIK 192
 DB 181 YGEGFKMNTQYIK 193
 RESULT 11
 ID 024138 TOBAC PRELIMINARY; PRT; 193 AA.
 AC 024138;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE NtSarl protein.

GN Name=NtSAR1;
 OS Nicotiana tabacum (Common tobacco).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 CC asterids; lamids; Solanales; Solanaceae; Nicotiana.
 CC NCBI_TaxID=4097;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Bright Yellow 2;
 RA Takeuchi M., Tada M., Saito C., Yashiroda H., Nakano A.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the small GTPase superfamily.
 DR EMBL: D87821; BA013463.1; -; mRNA.
 DR HSSP: Q9QVY3; 1F6B.
 DR GO: GO:0005525; P:GTP binding; IEA.
 DR GO: GO:0006886; P:intracellular protein transport; IEA.
 DR GO: GO:0007264; P:small GTPase mediated signal transduction; IEA.
 DR InterPro: IPR006689; ARF/SAR.
 DR InterPro: IPR001806; Ras_crnsmfng.
 DR InterPro: IPR006687; SARI_GTP_bd.
 DR InterPro: IPR005225; Small_GTP_bd.
 DR Pfam: PF00025; Arf; 1.
 DR PRINTS: PR00449; RASTNSFRMG.
 DR PRINTS: PR00328; SARI_GTPBP.
 DR SMART: SM00178; SAR; 1.
 DR TIGRFAMs: TIGR00231; small_GTP; 1.
 DR PROSITE: PS01020; SARI; 1.
 KM GTP-binding; Nucleotide-binding.
 SQ SEQUENCE 193 AA; 21922 MW; 79F05343BF760A70 CRC64;
 Query Match 84.9%; Score 847.5; DB 2; Length 193;
 Best Local Similarity 81.3%; Pred. No. 1.8e-62;
 Matches 157; Conservative 24; Mismatches 11; Indels 1; Gaps 1;
 QY 1 MFLVDMFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHPOTQPTSEELS 60
 DB 1 MFLVDMFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHPOTQPTSEELS 60
 QY 61 INRVKFAFDLGGHTTARVWDYAKVDAIVLVDAVDEREFAESKKELDLSLSDSL 120
 DB 61 IGRKIFKAFDGLGQIARVWKDYAKVDAIVLVDAVDEREFAESKKELDLSLSDSLA 120
 QY 121 QVPLVLGNKIDIPYASSEDELRLFTGLT-MTTGKGTVNLGDSNIRPIEVFMCSIVRKMG 179
 DB 121 TVPFLILGNKIDIPYASSEDELRLHGLISNFTTGKGVLDVGSVNRPLEVFMCSIVRKMG 180
 QY 180 YGEGFKMNTQYIK 192
 DB 181 YGEGFKMNTQYIK 193
 RESULT 12
 ID 081695 AVEFA PRELIMINARY; PRT; 193 AA.
 AC 081695;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Ras-like small monomeric GTP-binding protein.
 GN Name=SAR1;
 OS Avena fatua (Wild oat).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 CC Aveneae; Avena.
 CC NCBI_TaxID=4499;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Cranston H.J., Johnson R.R., Chaverra M.E., Dyer W.B.;
 RT "Isolation and characterization of a cDNA encoding a sar-1 like
 RT monomeric GTP-binding protein in *Avena fatua* L.";
 RL Plant Sci. 145:75-81(1999).
 CC -1- SIMILARITY: Belongs to the small GTPase superfamily.
 DR EMBL: AF084005; AAC32610.1; -; mRNA.

DR PIR; T52095; T52095.
DR HSBP; Q9QY13; 1F6B.
DR Gramene; O81695; -.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0006886; P:intracellular protein transport; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR006689; ARF/SAR.
DR InterPro; IPR001806; Ras_cnsftrng.
DR InterPro; IPR006687; SAR1_GTP_bd.
DR InterPro; IPR005225; Small_GTP_bd.
DR Pfam; PF00025; Arf; 1.
DR PRINTS; PR00449; RASTRNSFRMG.
DR PRINTS; PR00328; SAR1GTPBP.
DR SMART; SM00178; SAR; 1.
DR TIGRFAMs; TIGR00231; small_gtp; 1.
DR PROSITE; PS01020; SAR1; 1.
DR GTP-binding; Nucleotide-binding.
DR SEQUENCE 193 AA; 22018 MW; 730C366691D014D8 CRC64;

Query Match 84.5%; Score 843.5; DB 2; Length 193;
Best Local Similarity 81.8%; Pred. No. 3.9e-62;
Matches 157; Conservative 22; Mismatches 12; Indels 1; Gaps 1;

QY 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHPTQYPTSEELS 60
DB 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVQHPTQYPTSEELS 60
QY 61 INRVKFAFDLGGHTIARRVWDYAKVDAIVYLVDADVDERPFAESKKEIDSLSDSL 120
DB 61 IGKIKFAFDLGGHTIARRVWDYAKVDAIVYLVDADVDERPFAESKKEIDSLSDSL 120
QY 121 QVPVLVGNKIDIPYASSEBELRFTLGL-TMTGKGTVNLGDSNIRPIEFVMSIVKMG 179
DB 121 NVPEFLVGNKIDIPYASSEBELRYHLGLSFTTGKGVNLCDSNVRLVLEVMCSIVKMG 180
QY 180 YGEGFKMNTQYIK 191
DB 181 YGEGFKMNTQYIK 192

RESULT 13

065007 MALDO PRELIMINARY; PRT; 193 AA.
AC 065007;

DR 01-AUG-1998 (TREMBlrel. 07, Created)
DR 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DR 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DR GTP-binding protein Sar1.
OS Malus domestica (Apple) (Malus sylvestris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosid 1; Rosales; Rosaceae; Maloideae; Malus.
OX NCBI_TaxID=3750;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Two day apple fruit;
RA Morris B., Kvarnheden A., Yao J.-L., Sutherland P., Atkinson R.,
Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: Belongs to the small GTPase superfamily.
CC EMBL; AF048825; AAC05127.1; -; mRNA.
DR PIR; T16993; T16993.
DR HSBP; P20606; 1M2O.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0006886; P:intracellular protein transport; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR006689; ARF/SAR.
DR InterPro; IPR001806; Ras_trnsftrng.
DR InterPro; IPR006687; SAR1_GTP_bd.
DR InterPro; IPR005225; Small_GTP_bd.
DR Pfam; PF00025; Arf; 1.
DR PRINTS; PR00449; RASTRNSFRMG.
DR PRINTS; PR00328; SAR1GTPBP.

DR SMART; SM00178; SAR; 1.
DR TIGRFAMs; TIGR00231; small_gtp; 1.
DR PROSITE; PS01020; SAR1; 1.
DR GTP-binding; Nucleotide-binding.
DR SEQUENCE 193 AA; 21949 MW; B8E07A70D783B50B CRC64;

Query Match 83.7%; Score 835.5; DB 2; Length 193;
Best Local Similarity 81.9%; Pred. No. 1.8e-61;
Matches 158; Conservative 18; Mismatches 16; Indels 1; Gaps 1;

QY 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHPTQYPTSEELS 60
DB 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVQHPTQYPTSEELS 60
QY 61 INRVKFAFDLGGHTIARRVWDYAKVDAIVYLVDADVDERPFAESKKEIDSLSDSL 120
DB 61 IGKIKFAFDLGGHTIARRVWDYAKVDAIVYLVDADVDERPFAESKKEIDSLSDSL 120
QY 121 QVPVLVGNKIDIPYASSEBELRFTLGL-TMTGKGTVNLGDSNIRPIEFVMSIVKMG 179
DB 121 AVPEFLVGNKIDIPYASSEBELRFTLGLNFTTGKGVNLCDSNVRLVLEVMCSIVKMG 180
QY 180 YGEGFKMNTQYIK 192
DB 181 YGEGFKMNTQYIK 193

RESULT 14
024113 NICPL PRELIMINARY; PRT; 194 AA.
AC 024113;

DR 01-JAN-1998 (TREMBlrel. 05, Created)
DR 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DR 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DR Small GTP-binding protein.
OS Nicotiana glauca (leadwort-leaved tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4092;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Borlaug N.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the small GTPase superfamily.
DR EMBL; Y08424; CA69700.1; -; mRNA.
DR PIR; T16966; T16966.
DR HSBP; Q9QY13; 1F6B.

DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0006886; P:intracellular protein transport; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR006689; ARF/SAR.
DR InterPro; IPR001806; Ras_trnsftrng.
DR InterPro; IPR006687; SAR1_GTP_bd.
DR InterPro; IPR005225; Small_GTP_bd.
DR Pfam; PF00025; Arf; 1.
DR PRINTS; PR00449; RASTRNSFRMG.
DR PRINTS; PR00328; SAR1GTPBP.
DR SMART; SM00178; SAR; 1.
DR TIGRFAMs; TIGR00231; small_gtp; 1.
DR GTP-binding; Nucleotide-binding.
DR SEQUENCE 194 AA; 22032 MW; B6FB2630A5D4F3F CRC64;

Query Match 83.4%; Score 832; DB 2; Length 194;
Best Local Similarity 80.9%; Pred. No. 3.6e-61;
Matches 157; Conservative 22; Mismatches 13; Indels 2; Gaps 2;

QY 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHPTQYPTSEELS 60
DB 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVQHPTQYPTSEELS 60
QY 61 INRVKFAFDLGGHTIARRVWDYAKVDAIVYLVDADVDERPFAESKKEIDSLSDSL 120
DB 61 INRVKFAFDLGGHTIARRVWDYAKVDAIVYLVDADVDERPFAESKKEIDSLSDSL 120

Db 61 IGIKFKAFDLGSHQIARRVWKDYAKVDVAVYLVDVAYDKERFESKEKELDALLSDPSLA 120
Qy 121 QPVVVLGNKIDIPYASSSEDELFRTGLT-MTTGKGVNLGDSNIRPIEVMCSIVRK 179
Db 121 TVPFLILGNKIDIPYASSSEDELFRTGLTGTGGKGVNLAEISNVAPLEVMCSIVRK 180
Qy 180 -YEGEGFKMMTOYIK 192
Db 181 MGYGEGFKMVSQYIK 194

RESULT 15

SAR1B BRACM

ID SAR1B BRACM STANDARD; PRT; 195 AA.

AC 004267;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE GTP-binding protein SAR1B.

GN Name=SAR1B;

OS Brassica campestris (field mustard).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

OC rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

OX NCBI_TaxID=3711;

RN [1]

NP NUCLEOTIDE SEQUENCE.

RX MEDLINE=97299835; Pubmed=9154984; DOI=10.1023/A:1005731209124;

RA Kim W.Y., Cheong N.B., Je D.Y., Kim M.G., Lim C.O., Bahk J.D.,

RA Cho M.Y., Lee S.Y.;

RT "The presence of a Sar1 gene family in Brassica campestris that

suppresses a yeast vesicular transport mutation Sec12-1.";

RL Plant Mol. Biol. 33:1025-1035(1997).

CC -1- FUNCTION: Involved in transport from the endoplasmic reticulum to

the Golgi apparatus (By similarity).

CC -1- TISSUE SPECIFICITY: Expressed in most tissues.

CC -1- SIMILARITY: Belongs to the small GTPase superfamily, SAR1 family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL: U55036; AAC49717.1; -; mRNA.
DR HSSP: Q9GVY3; 1F6B.

DR InterPro: IPR006689; ARF/SAR.
DR InterPro: IPR001806; Ras trnsfmg.

DR InterPro: IPR006687; SAR1_GTP_bd.
DR InterPro: IPR005225; Small_GTP_bd.

DR PANTHER: PTHR11711; ARF/SAR; 1.
DR Pfam: PF00025; Arf; 1.

DR PRINTS: PR00449; RASTRNSFRNG.
DR PRINTS: PR00328; SAR1GTPBP.

DR SMART: SM00178; SAR; 1.

DR TIGRFSMs: TIGR00231; small_GTP; 1.

DR PROSITE: PS01020; SAR1; 1.

KW Endoplasmic reticulum; ER-Golgi transport; Golgi stack; GTP-binding;

KW Nucleotide-binding; Protein transport; Transport.

FT NP_BIND 27 34 GTP (By similarity).

FT NP_BIND 70 73 GTP (By similarity).

FT NP_BIND 129 132 GTP (By similarity).

FT NP_BIND 132 132 GTP (By similarity).

FT NP_BIND 129 132 GTP (By similarity).

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Qy 178 MGYGEGFKMMTOYI 191
Db 181 MGYGEGFKMVSQYI 194

Search completed: December 9, 2005, 01:37:53
Job time : 161 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 9, 2005, 01:28:26 ; Search time 43 Seconds
(without alignments)
369.157 Million cell updates/sec

Title: US-10-688-481-11

Perfect score: 998
Sequence: 1 MFLVDMFYGFYGLASIGLMQKE.....SIVRKMGYGEFGKMTQYIK 192Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	998	100.0	192	2	US-09-828-310-11 Sequence 11, Appl
2	614.5	61.6	198	1	US-08-825-780-1 Sequence 1, Appl
3	614.5	61.6	199	2	US-09-149-476-455 Sequence 455, Appl
4	593.5	59.5	193	1	US-08-825-780-4 Sequence 4, Appl
5	585.5	58.7	187	2	US-09-248-796A-20325 Sequence 20325, A
6	575.5	57.7	198	1	US-08-825-780-3 Sequence 3, Appl
7	386	38.7	86	2	US-09-621-976-4318 Sequence 4318, Ap
8	355	35.6	121	2	US-09-621-976-4305 Sequence 4305, Ap
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10	277	27.8	181	2	US-09-439-410A-53 Sequence 53, Appl
11	274.5	27.5	186	2	US-09-949-016-9065 Sequence 9065, Ap
12	260	26.1	152	2	US-09-270-767-32983 Sequence 32983, A
13	257.5	25.8	175	2	US-09-103-359-14 Sequence 14, Appl
14	257.5	25.8	179	1	US-08-049-473-32 Sequence 32, Appl
15	257.5	25.8	179	1	US-08-312-648-32 Sequence 32, Appl
16	257.5	25.8	179	4	PCT-US94-04190-32 Sequence 32, Appl
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18	246	24.3	156	2	US-09-621-976-4844 Sequence 4844, Ap
19	242.5	24.3	185	2	US-09-248-796A-20264 Sequence 20264, A
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21	240.5	24.1	181	1	US-08-312-648-29 Sequence 29, Appl
22	240.5	24.1	181	4	US-08-418-444A-4 Sequence 4, Appl
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24	240.5	24.1	215	2	US-09-949-016-10704 Sequence 10704, A
25	239.5	23.9	181	1	US-08-418-444A-7 Sequence 7, Appl
26	239	23.9	185	2	US-09-503-391-6 Sequence 6, Appl
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28	238.5	23.9	175	2	US-08-984-550-2 Sequence 2, Appl
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37	236	23.6	181	4	PCT-US94-04190-27 Sequence 27, Appl
38	236	23.6	217	2	US-09-949-016-8523 Sequence 8523, Ap
39	236	23.6	242	2	US-09-949-016-8306 Sequence 8306, Ap
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45	234	23.4	180	2	US-09-248-796A-19898 Sequence 19898, A

ALIGNMENTS

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RESULT 1
US-09-828-310-11
; Sequence 11, Application US/09828310
; Patent No. 6683938
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: BOHNETT, HANS J.
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
; FILE REFERENCE: IN PLANTS
; CURRENT APPLICATION NUMBER: US/09/828,310
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1.
; SEQ ID NO 11
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Physcomitrella patens
; US-09-828-310-11

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RESULT 2
US-08-825-780-1
; Sequence 1, Application US/08825780
; Patent No. 5834238
; GENERAL INFORMATION:
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; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purya
; TITLE OF INVENTION: NOVEL HUMAN GTP BINDING P
; TITLE OF INVENTION: ROTENIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,780
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PR-0264 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; LIBRARY: BRSTTUT14
; CLONE: 2742252
; US-08-825-780-1

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Best Local Similarity 59.0%; Pred. No. 1.66-60;
Matches 115; Conservative 36; Mismatches 39; Indels 5; Gaps 3;

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; Patent No. 6420526
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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08

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35	EARLIER APPLICATION NUMBER: 60/048,964
36	EARLIER FILING DATE: 1997-06-06
37	EARLIER APPLICATION NUMBER: 60/057,650
38	EARLIER FILING DATE: 1997-03-05
39	EARLIER APPLICATION NUMBER: 60/056,884
40	EARLIER FILING DATE: 1997-08-22
41	EARLIER APPLICATION NUMBER: 60/057,669
42	EARLIER FILING DATE: 1997-09-05
43	EARLIER APPLICATION NUMBER: 60/049,610
44	EARLIER FILING DATE: 1997-06-13
45	EARLIER APPLICATION NUMBER: 60/061,060
46	EARLIER FILING DATE: 1997-10-02
47	

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Best Local Similarity 59.0%; Pred. No. 1.6e-60;
Matches 115; Conservative 36; Mismatches 39; Indels 5; Gaps 3;

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          ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       63 ELTIAGMTFTTFDLGGHVAQRKRNKNTLPAINGLVPLVDCADHRLLESKEKELDSLMTDE 122
          ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

OY      118 LSLQVPLVLGNKKIDIPYASSEDELKFTLGL-TMTGKGVNLGDSNIRPIEFMCSIVR 176
          ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       123 TIANNPLTILGNKIDRPAISSEERLREMFGLVQGTGKGSISLKNLARNPLEVFMCSVLK 182
          ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

OY      177 KMGYGEQFKMTQYI 191
          :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       183 KQGYGEGRMAQYI 197
          :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 4
US-08-825-780-4
; Sequence 4, Application US/08825780
; Patent No. 5834238
; GENERAL INFORMATION:

```



```
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Shah, Purvi
/ TITLE OF INVENTION: NOVEL HUMAN GTP BINDING P
/ TITLE OF INVENTION: ROTENIN
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/825,780
/ FILING DATE: Filed Herewith
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0264 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 193 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 1326351
/ US-08-825-780-4

Query Match      59.5%; Score 593.5; DB 1; Length 193;
Best Local Similarity 56.0%; Pred. No. 3.4e-58;
Matches 107; Conservative 38; Mismatches 45; Indels 1; Gaps 1;

QY 2 FLVDMFGFLASISLGMKEAKILFLGLDNAGKTTLLHMLKDEKLGCHQHOPTVPTSELSI 61
DB 3 FLWMFNGVLMLGLANRKGKLVFLGLDNAGKTTLLHMLKDRLAQHVPFLHPTSELSI 62
QY 62 NRVEKFAFDLGHTIARRVMDYAKYDAIVYLVDAVDREFAESKKEIDSLSDSLQ 121
DB 63 GGISFTTYDLGHAQARVMDYFPAYDAVFLVDADAEHMOSSRYELSELDDDEQIAS 122
QY 122 VPVVLVGNKIDIPYASSEDELRFITGLT-MTTGKGTYNLGDNSIRPIEVFMCSTVRKMGY 180
DB 123 VPVVLVGNKIDIPYASSEDELRFITGLT-MTTGKGTYNLGDNSIRPIEVFMCSTVRKMGY 182
QY 181 GEGFKMTQYI 191
DB 183 GEGIRMLQYI 193

RESULT 5
US-09-248-796A-20325
/ Sequence 20325, Application US/09248796A
/ Patent No. 6747137
/ GENERAL INFORMATION:
/ APPLICANT: Keith Weinstein et al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
/ TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.112
/ CURRENT APPLICATION NUMBER: US/09/248,796A
```

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/ CURRENT FILING DATE: 1999-02-12
/ PRIOR APPLICATION NUMBER: US 60/074,725
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: US 60/096,409
/ PRIOR FILING DATE: 1998-08-13
/ NUMBER OF SEQ ID NOS: 28208
/ SEQ ID NO 20325
/ LENGTH: 187
/ TYPE: PRT
/ ORGANISM: Candida albicans
/ US-09-248-796A-20325

Query Match      58.7%; Score 585.5; DB 2; Length 187;
Best Local Similarity 63.0%; Pred. No. 2.5e-57;
Matches 114; Conservative 26; Mismatches 40; Indels 1; Gaps 1;

QY 11 LASIGLMOKEAKILFLGLDNAGKTTLLHMLKDEKLGCHQHOPTVPTSELSINRYKFAFD 70
DB 8 LSSDGLNNKAKLFLGLDNAGKTTLLHMLKDRLATLQPTLHPTSELSIGVRFITFD 67
QY 71 LGGHTIARRVMDYAKYDAIVYLVDAVDREFAESKKEIDSLSDSLQVPLVGNK 130
DB 68 LGCHQARRLMKDYFPEVNGIVFLVDADTERFAESKKEIDSLFRIEELSGVRFITFD 127
QY 131 IDIPYASSEDELRFITGLTMTTGKGTYNLGDNSIRPIEVFMCSTVRKMGYGEQFKMTQY 190
DB 128 IDVPTAVGEMELKNALGLVNTTGKDTGKLPDGT-RPIEVFMCSTVRKMGYGEQFKMTQY 186
QY 191 I 191
DB 187 I 187

RESULT 6
US-08-825-780-3
/ Sequence 3, Application US/08825780
/ Patent No. 5834238
/ GENERAL INFORMATION:
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Shah, Purvi
/ TITLE OF INVENTION: NOVEL HUMAN GTP BINDING P
/ TITLE OF INVENTION: ROTENIN
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/825,780
/ FILING DATE: Filed Herewith
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0264 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 198 amino acids
/ TYPE: amino acid
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RESULT 10
US-09-439-410A-53
; Sequence 53, Application US/09439410A
; Patent No. 6746852
; GENERAL INFORMATION:
; APPLICANT: Ciemowski, Mary
; APPLICANT: Duzic, Emil
; TITLE OF INVENTION: AGS PROTEIN AND NUCLEOTIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 1919/60388-B
; CURRENT APPLICATION NUMBER: US/09/439,410A
; CURRENT FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-439-410A-53

Query Match 27.8%; Score 277; DB 2; Length 181;
Best Local Similarity 34.8%; Pred. No. 7,7e-23;
Matches 65; Conservative 37; Mismatches 71; Indels 14; Gaps 3;

QY 9 GFLASIG--LMQEKALIFGLDNAGKTTLLHMLKDEKLGQHOPQYPTSELSINRVK 65
DB 3 GFFSSIFSSLFGRTEMILLILGLDAGKTTILYRLQVGEVVTITPTIGFNVETVYKRLK 62

QY 66 FKAPDLGHTIARVWRDYAKVDAIVLVDAVDRERFAESKEELSDLSLSDSLSOVPL 125
DB 63 FQVNDLGGQTSIRPYRCYNSNTDAIVYVDSQDRDRIGSKSLVAMLEEBELRLKILV 122

QY 126 VLGNKIDIPYASSEDELRTLTGTTGKTVNLGDSNIRPIEVFMCSIVKMGYGGGFK 185
DB 123 VFANKQMEQMTSEMANSLGLPA-----LKD---RKMQIFKTSATKGTGLDEAME 171

QY 186 WMTQYIK 192
DB 172 WLVELTK 178

RESULT 11
US-09-949-016-9065
; Sequence 9065, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFECTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9065
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9065

Query Match 27.5%; Score 274.5; DB 2; Length 186;
Best Local Similarity 33.3%; Pred. No. 1.5e-22;
Matches 63; Conservative 39; Mismatches 76; Indels 11; Gaps 2;

QY 2 FLVDMFYFLASIGLMQEKALIFGLDNAGKTTLLHMLKDEKLGQHOPQYPTSELSI 61
DB 9 FIMGFFSSIFSSLFGRTEMILLILGLDAGKTTILYRLQVGEVVTITPTIGFNVETVY 68

QY 62 NRVKFAFDIGHTIARVWRDYAKVDAIVLVDAVDRERFAESKEELSDLSLSDSLSO 121
DB 69 KNLFQVNDLGGQTSIRPYRCYNSNTDAIVYVDSQDRDRIGSKSLVAMLEEBELRK 128
QY 122 VPLVGNKIDIPYASSEDELRTLTGTTGKTVNLGDSNIRPIEVFMCSIVKMGYG 181
DB 129 AIIIVFANKQMEQMTSEMANSLGLPA-----LKD---RKMQIFKTSATKGTGLD 177

QY 182 EGFKMNTQY 190
DB 178 EAMEMQLKH 186

RESULT 12
US-09-270-767-32983
; Sequence 32983, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32983
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-32983

Query Match 26.1%; Score 260; DB 2; Length 152;
Best Local Similarity 40.5%; Pred. No. 4,7e-21;
Matches 53; Conservative 24; Mismatches 54; Indels 0; Gaps 0;

QY 18 QKEAKILFGLDNAGKTTLLHMLKDEKLGQHOPQYPTSELSINRVKFAFDIGHTIA 77
DB 19 EKEARILLGLDNAGKTTILKQLASEDITVTPTAGFNISVAADGPKLWMDIGQWKI 78

QY 78 RRVWRDYAKVDAIVLVDAVDRERFAESKEELSDLSLSDSLSOVPLVLGNKIDIPYAS 137
DB 79 RPYWKNYFANTDVILVICTDTRLEPAGSELFEMLMDRLKQVPLIFANKQMDPDM 138

QY 138 SEDELRTLTG 148
DB 139 SAAEVAEKMSL 149

RESULT 13
US-09-103-359-14
; Sequence 14, Application US/09103359
; Patent No. 6057108
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Guejler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Yue, Henry
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: HUMAN ARF-RELATED PROTEINS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Inocyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,359
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Carrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0537 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-855-0572
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: g178989
US-09-103-359-14

Query Match 25.8%; Score 257.5; DB 2; Length 175;
Best Local Similarity 35.6%; Pred. No. 1.1e-20;
Matches 64; Conservative 30; Mismatches 63; Indels 23; Gaps 7;

QY 19 KEAKILFLGDNAGKTTLLHMLKDEKLGQHPTQPT---SEELINRYKFAFDLGGH 74
DB 12 KERRILMLGDAAGKTTILYKL---KLGG-SVTITPTVGFRNVEVTYKYNKFNWVDVGGQ 67

QY 75 TIARVRDYAKVDAIVLVDAVDERFAESKKELDLSLDSQPVLYGNKIDIP 134
DB 68 DKIRPLMRHYTGTQGLIFVVDCAADRDRIDEARQELHRIINDEMRDAIILIFANKQDLP 127

QY 135 YASSEDELRTLLGTTMTGKTVNLGDSN--IRPIEFMCSIVRKNGYGGGFKMTQYIK 192
DB 128 DANKPHEIQEKGLT-----RIRDRNMYVGP---SCA-TSGDLVYGLTWLTSNYK 174

RESULT 14
US-08-049-473-32
Sequence 32, Application US/08049473
Patent No. 5386021
GENERAL INFORMATION:
APPLICANT: Moss, Joel
APPLICANT: Mishima, Koichi
APPLICANT: Nightingale, Maria
APPLICANT: Tsuchiya, Mikako
TITLE OF INVENTION: A MAMMALIAN GUANIN NUCLEOTIDE BINDING
TITLE OF INVENTION: PROTEIN WITH AN ADP-RIBOSYLATION FACTOR DOMAIN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
CITY: NEWPORT BEACH
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,473
FILING DATE: 19930419
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:

NAME: Fuller, Michael L.
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH050.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-049-473-32

Query Match 25.8%; Score 257.5; DB 1; Length 179;
Best Local Similarity 35.6%; Pred. No. 1.1e-20;
Matches 64; Conservative 30; Mismatches 63; Indels 23; Gaps 7;

QY 19 KEAKILFLGDNAGKTTLLHMLKDEKLGQHPTQPT---SEELINRYKFAFDLGGH 74
DB 16 KERRILMLGDAAGKTTILYKL---KLGG-SVTITPTVGFRNVEVTYKYNKFNWVDVGGQ 71

QY 75 TIARVRDYAKVDAIVLVDAVDERFAESKKELDLSLDSQPVLYGNKIDIP 134
DB 72 DKIRPLMRHYTGTQGLIFVVDCAADRDRIDEARQELHRIINDEMRDAIILIFANKQDLP 131

QY 135 YASSEDELRTLLGTTMTGKTVNLGDSN--IRPIEFMCSIVRKNGYGGGFKMTQYIK 192
DB 132 DANKPHEIQEKGLT-----RIRDRNMYVGP---SCA-TSGDLVYGLTWLTSNYK 178

RESULT 15
US-08-312-648-32
Sequence 32, Application US/08312648
Patent No. 5514600
GENERAL INFORMATION:
APPLICANT: Moss, Joel
APPLICANT: Mishima, Koichi
APPLICANT: Nightingale, Maria
APPLICANT: Tsuchiya, Mikako
TITLE OF INVENTION: A MAMMALIAN GUANIN NUCLEOTIDE BINDING
TITLE OF INVENTION: PROTEIN WITH AN ADP-RIBOSYLATION FACTOR DOMAIN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
CITY: NEWPORT BEACH
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/312,648
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,473
FILING DATE: 19-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael L.
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH050.001DVI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176

;/ INFORMATION FOR SEQ ID NO: 32:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 179 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ HYPOTHEICAL: NO
;/ ANTI-SENSE: NO
;/ FRAGMENT TYPE: N-terminal
;/ US-08-312-648-32

Query Match 25.8%; Score 257.5; DB 1; Length 179;

Best Local Similarity 35.6%; Pred. No. 1.1e-20;
Matches 64; Conservative 30; Mismatches 63; Indels 23; Gaps 7;

QY 19 KEAKILFLGLDNAGKTLTLHMLKDEKLGQHQPOTPT----SEELSIINRYKFAFDLGGH 74
Db 16 KEMRIIMGLDPAAGKTTILYKL--KLGG-SVTIIPVGFNVETVTKNVKFNWMDVGGQ 71
QY 75 TIARRVWRDYYAKVDIVLVDAVDRERFAESKKELDLSLSDSLSQVPVLGNKIDIP 134
Db 72 DKIRPLMRHHYVTGQGLIFVVDCAHDRIDEARQELHRIINDREMDAILILIFANKQDLR 131
QY 135 YASSEDELRLFTLGLTMTTGKGTNLGDSN--IRPIEVFMCSIVRKMGYGSGFKMMTOYIK 192
Db 132 DAMKPHSIQEKLGLT-----RIRDNMWVQP---SCA-TSGDGLYEGLTWLTSNYK 178

Search completed: December 9, 2005, 01:39:36
Job time : 44 secs

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OM protein - protein search, using sw model

Run on: December 9, 2005, 01:32:46 ; Search time 115 Seconds
(without alignments)
697.593 Million cell updates/sec

Title: US-10-688-481-11

Perfect score: 998
Sequence: 1 MFLVDMFYGLASIGLMQKE.....SIVRKMYGEGFKMTQYIK 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/us07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/us08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/us09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/us10A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	998	100.0	192	3	US-09-828-310-11 Sequence 11, Appl
2	998	100.0	192	4	US-10-688-481-11 Sequence 11, Appl
3	880.5	88.2	193	4	US-10-425-115-283016 Sequence 283016,
4	880.5	88.2	193	4	US-10-425-115-283017 Sequence 283017,
5	880.5	88.2	225	4	US-10-425-114-70682 Sequence 70682, A
6	880.5	88.2	229	4	US-10-425-114-71236 Sequence 71236, A
7	880.5	88.2	236	4	US-10-425-114-61506 Sequence 61506, A
8	877.5	87.9	193	4	US-10-767-701-45369 Sequence 45369, A
9	872.5	87.4	193	4	US-10-437-963-147565 Sequence 147565,
10	867.5	86.9	255	4	US-10-425-114-64729 Sequence 64729, A
11	862.5	86.4	193	4	US-10-424-599-156357 Sequence 156357,
12	862.5	86.4	193	4	US-10-767-701-66953 Sequence 66953, A
13	862.5	86.4	193	4	US-10-425-115-128003 Sequence 328003,
14	862.5	86.4	193	4	US-10-425-115-128005 Sequence 328005,
15	862.5	86.4	193	4	US-10-425-115-128006 Sequence 328006,
16	862.5	86.4	208	4	US-10-425-114-51042 Sequence 51042, A
17	862.5	86.4	236	4	US-10-425-114-63253 Sequence 63253, A
18	862.5	86.4	244	4	US-10-425-114-63253 Sequence 63253, A
19	862.5	86.4	251	4	US-10-425-114-50586 Sequence 50586, A
20	862.5	86.4	280	4	US-10-425-114-66257 Sequence 66257, A
21	859.5	86.1	193	4	US-10-424-599-156355 Sequence 156355,
22	859.5	86.1	266	4	US-10-425-114-45208 Sequence 45208, A
23	858.5	86.0	193	4	US-10-425-115-328001 Sequence 328001,
24	856.5	85.8	193	4	US-10-424-599-174038 Sequence 174038,
25	856.5	85.8	193	4	US-10-424-599-182648 Sequence 182648,
26	852.5	85.4	193	4	US-10-437-963-160822 Sequence 160822,
27	843.5	84.5	193	4	US-10-424-599-175209 Sequence 175209,

28	836.5	83.8	191	4	US-10-424-599-175210 Sequence 175210,
29	820.5	82.2	277	4	US-10-437-963-147566 Sequence 147566,
30	789.5	79.1	195	4	US-10-424-599-285372 Sequence 285372,
31	758	76.0	219	4	US-10-437-963-123137 Sequence 123137,
32	744.5	74.6	193	4	US-10-425-115-328658 Sequence 328658,
33	674.5	67.6	193	6	US-11-097-143-15609 Sequence 15609, A
34	665.5	66.7	154	4	US-10-425-115-197017 Sequence 197017,
35	627	62.8	189	4	US-10-128-714-8426 Sequence 8426, Ap
36	615	61.6	189	4	US-10-128-714-8426 Sequence 8426, Ap
37	614.5	61.6	199	3	US-09-809-391-455 Sequence 455, App
38	614.5	61.6	199	3	US-09-882-171-455 Sequence 455, App
39	614.5	61.6	199	4	US-10-164-861-455 Sequence 7773, Ap
40	613.5	61.5	190	4	US-10-032-585-7773 Sequence 158424,
41	612.5	61.4	149	4	US-10-437-963-158424 Sequence 158424,
42	599	60.0	191	4	US-10-320-797-3031 Sequence 3031, Ap
43	593.5	59.5	193	4	US-10-369-493-5976 Sequence 5976, Ap
44	586.5	58.8	198	5	US-10-719-993-472 Sequence 472, App
45	586.5	58.8	198	5	US-10-719-993-473 Sequence 473, App

ALIGNMENTS

```
RESULT 1
US-09-828-310-11
; Sequence 11, Application US/09828310
; Patent No. US20020066124A1
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSMALDO DA
; APPLICANT: BOHNETT, HANS J.
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
; FILE REFERENCE: 16313-0039
; CURRENT APPLICATION NUMBER: US/09/828,310
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Physcomitrella patens
; US-09-828-310-11

Query Match      100.0%; Score 998; DB 3; Length 192;
Best Local Similarity 100.0%; Pred. No. 4e-99;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MFLVDMFYGLASIGLMQKEAKLFLGLDNAGKTTLLHMLKDKRKGHOPTQYPTSELS 60
Db      1 MFLVDMFYGLASIGLMQKEAKLFLGLDNAGKTTLLHMLKDKRKGHOPTQYPTSELS 60

QY      61 INVKKRAFLGGHTTARVRDYAKVAIVLYLVADVBERPAESKKEJLSDLSLS 120
Db      61 INVKKRAFLGGHTTARVRDYAKVAIVLYLVADVBERPAESKKEJLSDLSLS 120

QY      121 QVPLVVGKIKIDIPYASSEDELFITGLTWTGKGTVNLGDSNIRPIEVMCSIVRMGY 180
Db      121 QVPLVVGKIKIDIPYASSEDELFITGLTWTGKGTVNLGDSNIRPIEVMCSIVRMGY 180

QY      181 GEGFKMTQYIK 192
Db      181 GEGFKMTQYIK 192

RESULT 2
US-10-688-481-11
; Sequence 11, Application US/10688481
; Publication No. US20040194163A1
; GENERAL INFORMATION:
```


APPLICANT: COSTA E SILVA, OSWALDO DA
APPLICANT: BOHNET, HANS J.
APPLICANT: VAN THIELEN, NOCHA
APPLICANT: CHEN, ROUYING
TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
TITLE OF INVENTION: IN PLANTS
FILE REFERENCE: 16313-0039
CURRENT APPLICATION NUMBER: US/10/688,481
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: 60/196,001
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 192
TYPE: PRT
ORGANISM: Physcomitrella patens
US-10-688-481-11

Query Match 100.0%; Score 998; DB 4; Length 192;
Best Local Similarity 100.0%; Pred. No. 4e-99;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHPTQYPTSELS 60
DB 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHPTQYPTSELS 60
QY 61 INRYKFAFDLGGHTIARRVWRDYAKVDAIVYLVDADVRRFAESKKEIDSLSDSL 120
DB 61 INRYKFAFDLGGHTIARRVWRDYAKVDAIVYLVDADVRRFAESKKEIDSLSDSL 120
QY 121 QVPVLVGNKIDIPYASSEDELRLFTLGLTMTGKGVNLDGNSNIRPIEFVFCISVRKMG 180
DB 121 QVPVLVGNKIDIPYASSEDELRLFTLGLTMTGKGVNLDGNSNIRPIEFVFCISVRKMG 180
QY 181 GEGFKMTQYIK 192
DB 181 GEGFKMTQYIK 192

RESULT 3

US-10-425-115-283016
Sequence 283016, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 283016
LENGTH: 193
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_21208C.1.pep
US-10-425-115-283016

Query Match 88.2%; Score 880.5; DB 4; Length 193;
Best Local Similarity 84.5%; Pred. No. 2e-86;
Matches 163; Conservative 19; Mismatches 10; Indels 1; Gaps 1;

QY 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHPTQYPTSELS 60
DB 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHPTQYPTSELS 60
QY 61 INRYKFAFDLGGHTIARRVWRDYAKVDAIVYLVDADVRRFAESKKEIDSLSDSL 120
DB 61 INRYKFAFDLGGHTIARRVWRDYAKVDAIVYLVDADVRRFAESKKEIDSLSDSL 120

DB 61 IGRIFKFAFDLGGHTIARRVWRDYAKVDAIVYLVDADVRRFAESKKEIDSLSDSLA 120
QY 121 QVPVLVGNKIDIPYASSEDELRLFTLGLTMTGKGVNLDGNSNIRPIEFVFCISVRKMG 179
DB 121 NVFPLVGNKIDIPYASSEDELRLFTLGLTMTGKGVNLDGNSNIRPIEFVFCISVRKMG 180
QY 180 YGEGFKMTQYIK 192
DB 181 YGEGFKMTQYIK 193

RESULT 4

US-10-425-115-283017
Sequence 283017, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 283017
LENGTH: 193
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_21209C.1.pep
US-10-425-115-283017

Query Match 88.2%; Score 880.5; DB 4; Length 193;
Best Local Similarity 84.5%; Pred. No. 2e-86;
Matches 163; Conservative 19; Mismatches 10; Indels 1; Gaps 1;

QY 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHPTQYPTSELS 60
DB 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHPTQYPTSELS 60
QY 61 INRYKFAFDLGGHTIARRVWRDYAKVDAIVYLVDADVRRFAESKKEIDSLSDSL 120
DB 61 IGRIFKFAFDLGGHTIARRVWRDYAKVDAIVYLVDADVRRFAESKKEIDSLSDSLA 120
QY 121 QVPVLVGNKIDIPYASSEDELRLFTLGLTMTGKGVNLDGNSNIRPIEFVFCISVRKMG 179
DB 121 NVFPLVGNKIDIPYASSEDELRLFTLGLTMTGKGVNLDGNSNIRPIEFVFCISVRKMG 180
QY 180 YGEGFKMTQYIK 192
DB 181 YGEGFKMTQYIK 193

RESULT 5

US-10-425-114-70682
Sequence 70682, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 70682


```

; LENGTH: 225
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3354-056-D12_FLI.pep
; US-10-425-114-70682

Query Match
Best Local Similarity 88.2%; Score 880.5; DB 4; Length 225;
Matches 163; Conservative 19; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MFLVDFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSELS 60
Db 33 MFLVDFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVGHOPTQYPTSELS 92
Qy 61 INRVKFAFDLGGHTTARRVWDYAKVDAIVYLVDVDERPFAESKKEIDSLSDSL 120
Db 93 IGRIFKFAFDLGGHQAIRRVWKDYAKVDAVVYLVDVDERPFAESKKEIDSLADSLA 152
Qy 121 QVPVLVGNKIDIPYASSEBELRFTGLT-MTTGKGTVNGDSNIRPIEVFMCISVRKM 179
Db 153 NVPEFLIGNKIDIPYASSEBELRYTGLSNFTGKGNVLADSNVRPLEIFMCSVVRKM 212
Qy 180 YGEGFKMMTOYIK 192
Db 213 YGEGFKMMTOYIK 225

RESULT 6
US-10-425-114-71236
; Sequence 71236, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaka, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425, 114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 71236
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-2MFLMO17103E09_FLI.pep
; US-10-425-114-71236

Query Match
Best Local Similarity 88.2%; Score 880.5; DB 4; Length 229;
Matches 163; Conservative 19; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MFLVDFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSELS 60
Db 37 MFLVDFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVGHOPTQYPTSELS 96
Qy 61 INRVKFAFDLGGHTTARRVWDYAKVDAIVYLVDVDERPFAESKKEIDSLSDSL 120
Db 97 IGRIFKFAFDLGGHQAIRRVWKDYAKVDAVVYLVDVDERPFAESKKEIDSLADSLA 156
Qy 121 QVPVLVGNKIDIPYASSEBELRFTGLT-MTTGKGTVNGDSNIRPIEVFMCISVRKM 179
Db 157 NVPEFLIGNKIDIPYASSEBELRYTGLSNFTGKGNVLADSNVRPLEIFMCSVVRKM 216
Qy 180 YGEGFKMMTOYIK 192
Db 217 YGEGFKMMTOYIK 229
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```

; LENGTH: 225
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3354-056-D12_FLI.pep
; US-10-425-114-70682

Query Match
Best Local Similarity 88.2%; Score 880.5; DB 4; Length 225;
Matches 163; Conservative 19; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MFLVDFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSELS 60
Db 33 MFLVDFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVGHOPTQYPTSELS 92
Qy 61 INRVKFAFDLGGHTTARRVWDYAKVDAIVYLVDVDERPFAESKKEIDSLSDSL 120
Db 93 IGRIFKFAFDLGGHQAIRRVWKDYAKVDAVVYLVDVDERPFAESKKEIDSLADSLA 152
Qy 121 QVPVLVGNKIDIPYASSEBELRFTGLT-MTTGKGTVNGDSNIRPIEVFMCISVRKM 179
Db 153 NVPEFLIGNKIDIPYASSEBELRYTGLSNFTGKGNVLADSNVRPLEIFMCSVVRKM 212
Qy 180 YGEGFKMMTOYIK 192
Db 213 YGEGFKMMTOYIK 225

RESULT 6
US-10-425-114-71236
; Sequence 71236, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaka, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425, 114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 71236
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-2MFLMO17103E09_FLI.pep
; US-10-425-114-71236

Query Match
Best Local Similarity 88.2%; Score 880.5; DB 4; Length 229;
Matches 163; Conservative 19; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MFLVDFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSELS 60
Db 37 MFLVDFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVGHOPTQYPTSELS 96
Qy 61 INRVKFAFDLGGHTTARRVWDYAKVDAIVYLVDVDERPFAESKKEIDSLSDSL 120
Db 97 IGRIFKFAFDLGGHQAIRRVWKDYAKVDAVVYLVDVDERPFAESKKEIDSLADSLA 156
Qy 121 QVPVLVGNKIDIPYASSEBELRFTGLT-MTTGKGTVNGDSNIRPIEVFMCISVRKM 179
Db 157 NVPEFLIGNKIDIPYASSEBELRYTGLSNFTGKGNVLADSNVRPLEIFMCSVVRKM 216
Qy 180 YGEGFKMMTOYIK 192
Db 217 YGEGFKMMTOYIK 229

RESULT 7
US-10-425-114-61506
; Sequence 61506, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaka, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425, 114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 61506
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB143-001-F4_FLI.pep
; US-10-425-114-61506

Query Match
Best Local Similarity 88.2%; Score 880.5; DB 4; Length 236;
Matches 163; Conservative 19; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MFLVDFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSELS 60
Db 44 MFLVDFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVGHOPTQYPTSELS 103
Qy 61 INRVKFAFDLGGHTTARRVWDYAKVDAIVYLVDVDERPFAESKKEIDSLSDSL 120
Db 104 IGRIFKFAFDLGGHQAIRRVWKDYAKVDAVVYLVDVDERPFAESKKEIDSLADSLA 163
Qy 121 QVPVLVGNKIDIPYASSEBELRFTGLT-MTTGKGTVNGDSNIRPIEVFMCISVRKM 179
Db 164 NVPEFLIGNKIDIPYASSEBELRYTGLSNFTGKGNVLADSNVRPLEIFMCSVVRKM 223
Qy 180 YGEGFKMMTOYIK 192
Db 224 YGEGFKMMTOYIK 236

RESULT 8
US-10-767-701-45369
; Sequence 45369, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5353)B
; CURRENT APPLICATION NUMBER: US/10/767, 701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 45369
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C2820_1.pap
; US-10-767-701-45369

Query Match
Best Local Similarity 87.9%; Score 877.5; DB 4; Length 193;
Matches 163; Conservative 19; Mismatches 10; Indels 1; Gaps 1;
```



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QY      1 MFLVDMFYGFPLASIGLMQKSAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQYPTSEELS 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 MFLVDMFYGFVLASIGLMQKSAKILFLGLDNAGKTTLLHMLKDEKLVQHOPQYPTSEELS 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      61 INRVKFAFDLGGHTIARRVWRDYAKVDAIVYLVDADVDERPAESKKEIDSLSDSLS 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 IGRKFAFDLGGHTIARRVWRDYAKVDAIVYLVDADVDERPAESKKEIDSLSDSLSLA 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      121 QVPLVLGNKIDIPYASSEBELRFTLGLT-MTTGKGVNLDGDSNIRPIEFVMSIVAKMG 179
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      121 NVPLLLGNKIDIPYASSEBELRYHGLSNFTTOKGKVNLDGDSNVRLPLVFMCSVYAKMG 180
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      180 YGEGFKMWTQYIK 192
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      181 YGEGFKMWSQYIK 193
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```

RESULT 9
US-10-437-963-147565
; Sequence 147565, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Mu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 147565
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURES:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_48081C.1.pep
US-10-437-963-147565

```

```

Query Match      87.4%; Score 872.5; DB 4; Length 193;
Best Local Similarity 83.4%; Pred. No. 1.4e-85;
Matches 161; Conservative 20; Mismatches 11; Indels 1; Gaps 1;

QY      1 MFLVDMFYGFPLASIGLMQKSAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQYPTSEELS 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 MFLVDMFYGVLASIGLMQKSAKILFLGLDNAGKTTLLHMLKDEKLVQHOPQYPTSEELS 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      61 INRVKFAFDLGGHTIARRVWRDYAKVDAIVYLVDADVDERPAESKKEIDSLSDSLS 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 IGRKFAFDLGGHTIARRVWRDYAKVDAIVYLVDADVDERPAESKKEIDSLSDSLSLA 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      121 QVPLVLGNKIDIPYASSEBELRFTLGLT-MTTGKGVNLDGDSNIRPIEFVMSIVAKMG 179
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      121 TVPPLLLGNKIDIPYASSEBELRYHGLSNFTTOKGKVNLDGDSNVRLPLVFMCSVYAKMG 180
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      180 YGEGFKMWTQYIK 192
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      181 YGEGFKMWSQYIK 193
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```

RESULT 10
US-10-425-114-64729
; Sequence 64729, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingtong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.

```

```

; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 64729
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURES:
; OTHER INFORMATION: Clone ID: LIB4606-001-A8_FLI.pep
US-10-425-114-64729

```

```

Query Match      86.9%; Score 867.5; DB 4; Length 255;
Best Local Similarity 83.4%; Pred. No. 7.3e-85;
Matches 161; Conservative 19; Mismatches 12; Indels 1; Gaps 1;

QY      1 MFLVDMFYGFPLASIGLMQKSAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQYPTSEELS 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      63 MFLVDMFYGVLASIGLMQKSAKILFLGLDNAGKTTLLHMLKDEKLVQHOPQYPTSEELS 122
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      61 INRVKFAFDLGGHTIARRVWRDYAKVDAIVYLVDADVDERPAESKKEIDSLSDSLS 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      123 IGRKFAFDLGGHTIARRVWRDYAKVDAIVYLVDADVDERPAESKKEIDSLSDSLSLA 182
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      121 QVPLVLGNKIDIPYASSEBELRFTLGLT-MTTGKGVNLDGDSNIRPIEFVMSIVAKMG 179
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      183 NVPLLLGNKIDIPYASSEBELRYHGLSNFTTOKGKVNLDGDSNVRLPLVFMCSVYAKMG 242
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      180 YGEGFKMWTQYIK 192
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      243 YGEGFKMWSQYIK 255
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```

RESULT 11
US-10-424-599-156357
; Sequence 156357, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 156357
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURES:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_112210C.1.pep
US-10-424-599-156357

```

```

Query Match      86.4%; Score 862.5; DB 4; Length 193;
Best Local Similarity 82.9%; Pred. No. 1.7e-84;
Matches 160; Conservative 20; Mismatches 12; Indels 1; Gaps 1;

QY      1 MFLVDMFYGFPLASIGLMQKSAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQYPTSEELS 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 MFLVDMFYGVLASIGLMQKSAKILFLGLDNAGKTTLLHMLKDEKLVQHOPQYPTSEELS 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      61 INRVKFAFDLGGHTIARRVWRDYAKVDAIVYLVDADVDERPAESKKEIDSLSDSLS 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 IGRKFAFDLGGHTIARRVWRDYAKVDAIVYLVDADVDERPAESKKEIDSLSDSLSLA 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```



```

Oy      121  QVPVLVANKKIDIPASSEDELRFTGLT-MTTGKGVNLGDSNIRPIEFVCSIVKKG 179
Db      121  TVPFLILNKKIDIPASSEELRLHGLNFTTGKGVNLSDSNVREVEFVCSIVKKG 180
Oy      180  YGEGFKWMTQYIK 192
Db      181  YGDFKWLQYIK 193

RESULT 12
US-10-767-701-46953
: Sequence 46953, Application US/10767701
: Publication No. US20040172684A1
: GENERAL INFORMATION:
: APPLICANT: Kovalic, David K.
: APPLICANT: Zhou, Yihua
: APPLICANT: Cao, Yongwei
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
: FILE REFERENCE: 38-21(5353)B
: CURRENT APPLICATION NUMBER: US/10/767, 701
: CURRENT FILING DATE: 2004-01-29
: NUMBER OF SEQ ID NOS: 63128
: SEQ ID NO 46953
: LENGTH: 193
: TYPE: PRT
: ORGANISM: Sorghum bicolor
: FEATURE:
: OTHER INFORMATION: Clone ID: SORBI-28MAV03-C49_287 деп
: US-10-767-701-46953

```

```

Query Match 86.4%; Score 862.5; DB 4; Length 193;
Best Local Similarity 82.8%; Pred. No. 1.7e-84;
Matches 159; Conservative 22; Mismatches 10; Indels 1; Gaps 1;

QY      1 MFLVDYFPGFLASISGLMOKKAKILPLGLDNAGKTLILHMLKDBKLGQHOPTQPTPSSEIS 60
Db      1 MFLVDYFPGVIVLASISLIMOKKAKILPLGLDNAGKTLILHMLKDBRLVQHOPTQPTPSSEIS 60

QY      61 INRVFKAFDGLGHTIARVWRDYAKVDAYLYLVDAVVRERPAESKKEIDSLSDSIS 120
Db      61 IGRIFKAFDGLGHTIARVWRDYAKVDAYLYLVDAVYKERPAESKKEIDSLSDSIS 120

QY      121 QVPVLVIGNKIDIPYASSEDELFTLGLT-MTTGKTGVLGDSNIRPIEFVFCISVRKXG 179
Db      121 TVPFLILGNKIDIPYAAASEEELRYHMGLSNFTTGKGVNLGDSNVAPLEVFVFCISVVRKXG 180

QY      180 YGEGFKMTQYI 191
Db      181 YGDGFKWVSQYI 192

RESULT 13
US-10-425-115-328003
: Sequence 328003, Application US/10425115
: Publication NO. US20040214272A1
: GENERAL INFORMATION:
: APPLICANT: La Rosa, Thomas J.
: APPLICANT: Kovalic, David K.
: APPLICANT: Zhou, Yihua
: APPLICANT: Cao, Yongwei
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants
: FILE REFERENCE: 38-21(53222)B
: CURRENT APPLICATION NUMBER: US/10/425,115
: NUMBER OF SEQ ID NOS: 2003-04-28
: SEQ ID NO 328003
: LENGTH: 193
: TYPE: PRT
: ORGANISM: Zea mays
: FEATURE:
: OTHER INFORMATION: Clone ID: MRT4577_62203C.1.pep

```

[illegible]

```

RESULT 14
US-10-425-115-328005
; Sequence 328005, Application US/10425115
; Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425.115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 328005
LENGTH: 193
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_62205C.1.pep
US-10-425-115-328005

Query Match      86.4%; Score 862.5; DB 4; Length 193;
Best Local Similarity 82.9%; Pred. No. 1.7e-84;
Matches 160; Conservative 21; Mismatches 11; Indels 1; Gaps 1;

QY      1 MELVDWFGFGLASTIGLMOKEAKITFLGIDNAGKTTLLHMLKDExLGQHOPPTSEELS 60
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       1 MFLWDWFEGVLASIGLMQEKKITLFLGDNGKTTLLHMLKDERLVQHOPPTSEELS 60
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      61 INRYEKAFFDLGGHTIARVRDYYAKYDAIVYLVDADVDRERFAESKKELDISLSDSIS 120
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       61 IGRIKFKAFDLGGHQIARVWKDYAKVDVVYLVDADVKERFAESKKELDALSLSDSILA 120
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      121 QVEPLVLGNKKTIDIPYASEDELRFTLGIT-MTGGCTVNLGNSNRPIEFVFNCSYRKKG 179
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       121 NVPLILGNKKTIDIPYASEEBELRHYHLGSLNFTTGKYNLGSNSVRPLEVFNCSSVRKKG 180
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      180 YGEGFKNMTGYIK 192
        ||| ||| ||| |||
Db       181 YGDGFKWSQYIK 193
        ||| ||| ||| |||

RESULT 15
US-10-425-115-328006
; Sequence 328006, Application US/10425115
; Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
```



```
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 328006
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_62206C.1.pep
US-10-425-115-328006

Query Match      86.4%; Score 862.5; DB 4; Length 193;
Best Local Similarity 82.9%; Pred. No. 1.7e-84;
Matches 160; Conservative 21; Mismatches 11; Indels 1; Gaps 1;

QY      1 MFLVDMFYGFGLASIGLWOKBAKILFLGIDNAGKTTLLHMLKDEKLGQHOPTOYPTSELS 60
DB      1 MFLMDMFTYGVILASIGLWOKBAKILFLGIDNAGKTTLLHMLKDEKLVQHPTOYPTSELS 60

QY      61 INRVKFAFDLGGHTIARVRWDYAKVDAIVLVDAVDRERFAESKKELSDLSLSDSL 120
DB      61 IGKIKFAFDLGGHGIARVRWKDYAKVDAIVLVDAVDKRFASKKELDALSLSDSLA 120

QY      121 QVPVLVGNKTDIPYASSEDLRFTLGIL-MTGGKTVNLGDSNIRPIEVMCSIVRKMG 179
DB      121 NVPLILGNKTDIPYASSEELRYHLGSLNFTTGKGVNLGDSNVRLPLEVMCSIVRKMG 180

QY      180 YGEGFKMMTOYIK 192
DB      181 YGEGFKMVSQYIK 193
```

Search completed: December 9, 2005, 01:41:43
Job time : 117 secs


```

; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821.234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1078
; LENGTH: 242
; TYPE: PR1
; ORGANISM: Homo sapiens
; US-10-821-234-1078

```

Query Match	24.9%	Score 248.5;	DB 6;	Length 242;
Best Local Similarity	32.0%	Pred. No. 6,1e-18;		
Matches 62;	Conservative 31;	Mismatches 78;	Indels 23;	Gaps 4;

```

QY 3 LVMPFAGFLASIGLMOKEKXKIFLGLGNAGKTTLLHMLKDEKLOQHPQYPT-----SEE 58
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 64 LDMFSL-----FWKEBEMELTLVGLQYSKTTFNVIAS---QFSEDMLPTVGFMRK 115
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 59 LSINRYKFAFDLGGHTIARVWRDYAKVDAIVYLVDVADREBPASCKEKLSDLSDDS 118
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 116 VTKGNVTIKIMDIGQPRFSWMERXCGVNAIVYIMDAADREKIEASRNELHNLDPQ 175
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 119 LSGVPLVLGNKIDIDYASSEDELRPTGLTWTCTGKIVNIGDSNIPPIEVFMOSIVRKM 178
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 176 LQGIPLVLVGNKRDELNALDEKOL-----IEKNLSAIQDRBICCYSSICKED 224
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 179 GYGEGRKMTQYIK 192
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 225 NIDITLQWMLQHSK 238
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

```

RESULT 3
US-11-093-746A-22
Sequence 22, Application US/11093746A
Publication No. US20050266443A1
GENERAL INFORMATION:
APPLICANT: Cioce, Carlo M.
APPLICANT: Calin, George A.
TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
FILE REFERENCE: 3589.1015-003
CURRENT APPLICATION NUMBER: US/11/093,746A
CURRENT FILING DATE: 2005-03-30
PRIOR APPLICATION NUMBER: PCT/US2003/032270
PRIOR FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: 60/417,842
PRIOR FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 176
TYPE: PRT
ORGANISM: Mus musculus
US-11-093-746A-22

```

Query Match	23.2%	Score 232;	DB 7;	Length 176;
Best Local Similarity	36.7%	Pred. No. 1.7e-16;		
Matches 55;	Conservative 25;	Mismatches 56;	Indels 14;	Gaps 2

[illegible]

```

QY      139 EDELRFITGL-----TMTGKG 155
          | : |||
          | : |||
Db      132 LLEIRNRLLGEFGFKHCWELRACSAALTGG 161

```

```

RESULT 4
US-11-093-746A-23
: Sequence 23, Application US/11093746A
: Publication No. US20050266443A1
: GENERAL INFORMATION:
: APPLICANT: Croce, Carlo M.
: APPLICANT: Callin, George A.
: TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING AND USING THE SAME
: FILE REFERENCE: 3589.1015-003
: CURRENT APPLICATION NUMBER: US/11/093,746A
: CURRENT FILING DATE: 2005-03-30
: PRIOR APPLICATION NUMBER: PCT/US2003/032270
: PRIOR FILING DATE: 2003-10-10
: PRIOR APPLICATION NUMBER: 60/417,842
: PRIOR FILING DATE: 2002-10-11
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 23
: LENGTH: 173
: TYPE: PRT
: ORGANISM: Rattus norvegicus
US-11-093-746A-23

```

Query Match	22.4%	Score 224;	DB 7;	Length 173;
Best Local Similarity	34.6%	Pred. No. 1,1e-15;		
Matches 55; Conservative	27;	Mismatches 63;	Indels 14;	Gaps 2

```

Qy 11 AASIGLMQKXKELLFLGIDNKGKTLTLMLEDEKQGNQPTQYPSSELSI -NRVFKAF 69
Db 1 MGSVNSRCHKAQVYMLGIDLCAGKTTILYKLGKNNRLVDTLPVGFVNEPTEADGHSLTLM 60
Qy 70 DLGGHTTARRWRDYAKVDAIVYLVDAVDRERFAESKEKELDSLSDSLGQVPLVLGN 129
Db 61 DIGGQTQIRATWRYKYLEGIDILLVYLDSTDEARLEPAVALEEVLEADPMAGVPEPLVLAN 120
Qy 130 KIDIPYASSEDELRFTLGL-----TMTGKG 155
Db 121 KQEAADALPLIEIRNRDLERFQDHCWELRACASALTGGQ 159

```

```

RESULT 5
US-11-093-746A-21
; Sequence 21, Application US/11093746A
; Publication No. US20050266443A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Callin, George A.
; TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3589.1015-003
; CURRENT APPLICATION NUMBER: US/11/093,746A
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: PCT/US/003/032270
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/417,842
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-746A-21

```

Query Match	22.3%	Score 222.5;	DB 7;	Length 201;
Best Local Similarity	31.7%	Pred. No. 1.8e-15;		
Matches 57;	Conservative 34;	Mismatches 62;	Indels 27;	Gaps 3


```

Qy 22 IIFELGDNNGKTTLLHMLKDEKLGHOHPQVPTSELSI-----NRKFKRFLDGGHTIA 77
Db 24 VVVIIGDSDGAKTSLRLKFKFVQSPVPGKGTETIKIIVPLJGSGRGITFPQWMDVGGSEKL 83
Qy 78 RRVWRDYAKVAIVLVDAVDRERERPAESKKELDLSLSDSLSGQVPLVLGNKRIDIPYAS 137
Db 84 RPLMRSYNRRTDGLFVVDVAEAEERLEBEKVELHRIISASDNGQVPLVLANKDQDQAL 143
Qy 138 SEDELRFTTGL-----TWTTGKGVNLGDSNIRPIEVMCSIRKMGVGEGBFMMQYI 191
Db 144 SAAEVEKRLAVBELAAATITTHVQG-----CSAVDGLGQGGLERLVEMI 187

```

```

RESULT 6
US-11-093-746A-2
; Sequence 2, Application US/11093746A
; Publication No. US2005026643A1
; GENERAL INFORMATION:
; APPLICANT: Cioce, Carlo M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3589.1015-003
; CURRENT APPLICATION NUMBER: US/11/093,746A
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: PCT/US2003/032270
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/417,842
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-093-746A-2

```

[illegible]

```

RESULT 7
US-11-093-746A-26
: Sequence 26, Application US/11093746A
: Publication No. US20050266443A1
: GENERAL INFORMATION:
: APPLICANT: Croce, Carlo M.
: APPLICANT: Callin, George A.
: TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING AND USING THE SAME
: FILE REFERENCE: 3589.1015-003
: CURRENT APPLICATION NUMBER: US/11/093,746A
: CURRENT FILING DATE: 2005-03-30
: PRIOR APPLICATION NUMBER: PCT/US2003/032270
: PRIOR FILING DATE: 2003-10-10
: PRIOR APPLICATION NUMBER: 60/417,842
: PRIOR FILING DATE: 2002-10-11
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: FastSeq for Windows Version 4.0

```

```

; SEQ ID NO 26
;
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
;
US-11-093-746A-26

```

Query Match	21.7%	Score	216.5	DB 7	Length	205			
Best Local Similarity	29.9%	Pred. No.	7.4e-15						
Matches	52	Conservative	35	Mismatches	76	Indels	11	Gaps	1

```

Oy      16 QKAKILFLGIDNAGKTTLLHMLKDEKLGHQHPOTQYPISELSINRVKFRADFLSGHTIA 77
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      15 KSKRIILMWGHDGSGKTTILYKLLGEVTVTPTIGFNLETVKEYGINFTVMDIGQEKI 74

```

```
QY      76 RRWRDYYAKVDALVYLDAVDREHFAESKELDSLSDSLSQVPVLGVKKIDIPYAS 137
       11::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      75 RKLIRHYFQNAQGILFVVDSSDSERLSEARNELHLRILTITNELEGACVLFANKQDSRNAL 134
```

```

QY      138 SEDDELRLFTGLTMTTGKGTAVNIGDSNIRIEVFMSIVRKMGVGGGPKMTQYI 191
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      135 PVAEVANKLGLHSLSKRCWLIG-----TSAISGGGLYEGLEMLSTTI 177

```

```

RESULT 8
US-10-821-928
; Sequence 928, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labac, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methode for diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 928
; LENGTH: 202
;
; TYPE: PRT
;
; ORGANISM: Homo sapiens
US-10-821-928

```

Query Match	21.3%	Score	212.5	DB 6	Length	202;			
Best Local Similarity	30.1%	Pred. NO.	1.6e-14;						
Matches	52;	Conservative	33;	Mismatches	73;	Indels	15;	Gaps	2

[illegible]

```

RESULT 9
US-11-093-746A-24
; Sequence 24, Application US/11093746A
; Publication No. US20050266443A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3589.1015-003

```



```

; CURRENT APPLICATION NUMBER: US/11/093,746A
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: PCT/US2003/032270
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/417,842
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FaetsSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Danio rerio
US-11-093-746A-24

Query Match      20.4%; Score 204; DB 7; Length 176;
Best Local Similarity 30.2%; Pred. No. 1.1e-13;
Matches 51; Conservative 32; Mismatches 74; Indels 12; Gaps 2

QY 17 WQEKAKILFGLDGNAGKTTLLHMLDKDEKLGQHQPPTPYRSELSIN-RVKFAPDLGGHT 75
      ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 9 FKPKPQVLLMGDSAGKSTLMRKQLHGYMTQSPVGVFVATLQANKTSLTWIIGQD 68
      76 IARRVARDYAKVAIVLVDAVNDEREFAESKKELDLSLSDSLSOQPVLYGNKIDIPY 135
      69 TMRPMKKYLLBESCKYLVFVVDSSDYARIGEAGKALKITLHDEHLGVPMLVANKDLPN 128
QY 136 ASSEDELRFPTLGLTMTTGKGYTNLGDNSIRPLEVFMCSIVRRMGYGBGF 184
      129 TWIREVSTKLDLDITYTD-----RQWEIQACSAVKGLGLGQAF 166

RESULT 10
US-11-093-746A-19
; Sequence 19, Application US/11093746A
; Publication No. US2005026443A1
; GENERAL INFORMATION:
; APPLICANT: Croce, George M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3589.1015-003
; CURRENT APPLICATION NUMBER: US/11/093,746A
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: PCT/US2003/032270
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/417,842
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FaetsSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-746A-19

Query Match      19.4%; Score 193.5; DB 7; Length 200;
Best Local Similarity 31.6%; Pred. No. 1.4e-12;
Matches 54; Conservative 31; Mismatches 61; Indels 25; Gaps 5

QY 23 IIFGLDGNAGKTTLLHMLDKDEKLGQHQPPTPYRSELSI-----NRVKFAPDLGGHTIA 77
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 23 IYILGDCKGKTTVLRLLPNEVNTVPTKGFNTKIKITLNGSKTVTTHFMVDGQEKY 82
      78 RRRVARDYAKVAIVLVDAVNDEREFAESKKELDLSLSDSLSOQPVLYGNKIDIPYAS 137
      83 RLKMSYTCGTGIVFVVDSDVERNEEAKTELHKITRISENGQVPLVLVANKQDILRNSL 142
QY 138 SDEDELRFPTLGLTMTTGKGYTNLGDNSIRPLEVFMCSIVRRMGYGBGF 185
      143 SLSEIKLILAMG-----ELSSSTPMHLQPTCAII-----GDGLK 176

RESULT 11

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[illegible]


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DB 62 LQIMDAGGERFRTTSSYRGAGIIVYDVTDQESFNNVKQMLQEI DRVASEN-----V 117
QY 123 PVLVLGNKID-----IPYASSEDELRLFTLGLTM--TTGKGTYNLGDNSNIRPIEVFM--- 171
DB 118 NKLVLGNKCDLTKKVVDTYTK-EPADSLGIFPLETSKATNATVEOS-----FMTMA 169
QY 172 CSIVRKMGGY 181
DB 170 AEIKRMGPG 179

RESULT 13
US-10-821-234-1069
; Sequence 1069, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labac, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methode for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1069
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1069

Query Match 11.9%; Score 118.5; DB 6; Length 216;
Best Local Similarity 24.9%; Pred. No. 4.4e-05;
Matches 47; Conservative 28; Mismatches 63; Indels 51; Gaps 9;

QY 22 KILFLGIDNAGKTTLLHMLKDEKLGQHPTQYPTSELSINRV---KFAFPLGCHTIA 77
DB 25 KLLLIIGSGVSKSCLLRFADD-----TTYESYSTIGVDFKRTIILDGKTK 73
QY 78 RRVV-----RDYAKVDAYVLDVADVRERFAESK---KELDSLSDSLSOV 122
DB 74 LQIMDAGGERFRTTSSYRGAGIIVYDVTDQESFNNVKQMLQEI DRVASEN-----V 129
QY 123 PVLVLGNKIDIPYASSED-----ELRFTLGLTM--TTGKGTYNLGDNSNIRPIEVFM---C 172
DB 130 NKLVLGNKCDLTKKVVDTYTK-EPADSLGIFPLETSKATNATVE-----QAFMTMA 182
QY 173 SIVRKMGGY 181
DB 183 EIKRMGPG 191

RESULT 14
US-11-099-691-13
; Sequence 13, Application US/11099691
; Publication No. US20050260644A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: BANDMAN, Olga
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: LAL, Preeti
; APPLICANT: YUB, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: PATERSON, Chandra
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: YANG, Junming
; TITLE OF INVENTION: CELL SIGNALING PROTEINS
; FILE REFERENCE: PF-0521 PCT
; CURRENT APPLICATION NUMBER: US/11/099,691
; CURRENT FILING DATE: 2005-04-06
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; PRIOR APPLICATION NUMBER: US/09/700,444
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/085,343
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,010
; PRIOR FILING DATE: 1998-08-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte Clone 3315936
US-11-099-691-13

Query Match 10.0%; Score 100; DB 7; Length 123;
Best Local Similarity 28.8%; Pred. No. 0.0014;
Matches 23; Conservative 20; Mismatches 35; Indels 2; Gaps 1;

QY 70 DLGHTIARVRWDYAKVDAYVLDVADVRERFAESKELDSLSDSLSOVPVVLGN 129
DB 5 EIGGSKPFRSYWEMLYSKGLLIFVVDSDHSHRLPEAKKYLHQLIANPV--LPLVFN 62
QY 130 KIDIPYASSEDELRLFTLGLT 149
DB 63 KODLEAHYHTIDIEHALS 82

RESULT 15
US-10-821-234-1100
; Sequence 1100, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labac, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methode for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1100
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1100

Query Match 10.0%; Score 99.5; DB 6; Length 408;
Best Local Similarity 28.2%; Pred. No. 0.0079;
Matches 31; Conservative 16; Mismatches 38; Indels 25; Gaps 3;

QY 49 QPTQYPTSELSINRVK-----FKADLGGHTIARVRWDYAKVDAYV 93
DB 218 QSDYIPTQDDVLRTRKXTGIVETHFTFKDLHFKMPDVGGORSEKRWIHCFCGVYALIF 277
QY 94 -----LVDAVDR--RFAESKELDSLSDSLSOVPVVLGNKIDI 133
DB 278 CVALSAVDVLVAEDENRMHESMKLPDSICNNKWFDTGSIILPKKOD 327
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Search completed: December 9, 2005, 01:42:19
Job time : 26 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 01:38:47 ; Search time 3390 Seconds
(without alignments)
3219.452 Million cell updates/sec

Title: US-10-688-481-11

Perfect score: 998

Sequence: 1 MFVLVDFYGYGLASIGLMQKE.....SIVRKXMGYGRGPKMTQYIK 192

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	998	100.0	667	6	AR474309 Sequence
2	998	100.0	667	6	AX282608 Sequence
3	998	100.0	805	6	AR474304 Sequence

C	4	998	100.0	805	6	AX282603	AX282603 Sequence
5	876.5	87.8	945	15	AY596178	AY596178 Zea mays	
6	872.5	87.4	1035	15	AK119179	AK119179 Oryza sat	
7	872.5	87.4	1035	15	AK119548	AK119548 Oryza sat	
8	872.5	87.4	1049	15	AK111904	AK111904 Oryza sat	
9	872.5	87.4	1086	15	AY620417	AY620417 Oryza sat	
10	871.5	87.3	582	15	AF210431	AF210431 Nicotiana	
11	863.5	86.5	957	15	TOMGTPASE	L12051 Lycopersico	
12	862.5	86.4	613	15	AY096699	AY096699 Arabidops	
13	862.5	86.4	884	15	AY088765	AY088765 Arabidops	
14	862.5	86.4	899	15	AT056929	U56929 Arabidops	
15	862.5	86.4	926	15	AY065357	AY065357 Arabidops	
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17	860.5	86.2	927	15	AK099125	AK099125 Oryza sat	
18	860.5	86.2	952	15	AK060332	AK060332 Oryza sat	
19	856.5	85.8	934	15	AK099149	AK099149 Oryza sat	
20	854.5	85.6	966	15	NP3SARGTP	OY08423 N.plumbagin	
21	854.5	85.6	1031	15	BT012780	BT012780 Lycopersi	
22	853.5	85.5	613	15	AY117363	AY117363 Arabidops	
23	853.5	85.5	795	15	AY070378	AY070378 Arabidops	
24	852.5	85.4	1094	15	AK112012	Oryza sat	
25	852.5	85.4	1152	15	AK103351	AK103351 Oryza sat	
26	850.5	85.2	613	15	AY096599	AY096599 Arabidops	
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29	850.5	85.2	950	15	AY072220	AY072220 Arabidops	
30	848.5	85.0	857	15	BCU55035	U55035 Brassica ca	
31	847.5	84.9	1020	15	DB7821	D87821 Nicotiana t	
32	843.5	84.5	801	15	AF084005	AF084005 Avena fat	
33	835.5	83.7	709	15	NP50SAR	AF048825 Malus dom	
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36	822.5	82.4	613	15	AY090921	AY090921 Arabidops	
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38	758	76.0	760	15	AY620416	AY620416 Oryza sat	
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41	728.5	73.0	27502	15	ATAF001535	AF001535 Arabidops	
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ALIGNMENTS

RESULT 1
AR474309 LOCUS AR474309 667 bp DNA
DEFINITION Sequence 6 from patent US 6689939.
ACCESSION AR474309
VERSION AR474309.1 GI:42713157
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 667)
AUTHORS da Costa e Silva,O., Bohner,H.J., van Thiel,N., van Chen,R.
TITLE GTP binding stress-related proteins and methods of use in plants
JOURNAL Patent: US 6689939-A 6 10-FEB-2004;
BASF Plant Science GmbH; Ludwigshafen;
MOX;

FEATURES
source location/Qualifiers
1..667 /organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores: 1.14e-96 Length: 667
Pred. No.: 998.00 Matches: 192
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-688-481-11 (1-192) x AR474309 (1-667)

Qy 1 MetPheLeuValAspTTPPhetYrGlyPheLeuAlaSerIleGlyLeuTPGlnLyGlu 20
Db 33 ATGTTCTTGTAAGTGGTTTACGGCTTCTTCCGACATAGGGCTGTGGCAAAAGAG 92
Qy 21 AlAlaYsIleLeuPheLeuGlyLeuAspAsnAlaGlyYsThrThrLeuLeuHisMetLeu 40
Db 93 GCCAAATCCTGTTCTGGCTCGACAAATCTGGCAAGACTACTCTTTCGACATGCTC 152
Qy 41 LysAspGluYsLeuGlyGlnHisGlnProThrGlnTyrProThrsSerGluLeuSer 60
Db 153 AAGGATGAGAACTGGGGCAACATCAACCAACGAGATCAACGTCAGAGAGTTGAGT 212
Qy 61 IleAsnArgValIlyPheYsAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db 213 ATCAACAGAGTGAAGTTCMAAGCATTCGATCTGGTGGCCACAAATCGCTCGACGGTG 272
Qy 81 TrpArgAspTyrTyrAlaYsValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db 273 TGGAGGACTACTATGCTTAAGTGATGCTATAGTATCTCGTCGACGACGTAGACAG 332
Qy 101 GluArgPheAlaGluSerIlyYsGluLeuAspSerLeuSerAspAspSerLeuSer 120
Db 333 GAGAGATTGCTGATCAAGAAAGAGCTCGATTCCTCTCCGACGATTCCTGTCC 392
Qy 121 GlnValProValLeuValLeuGlyYsAsnYsIleAspIleProTyrAlaSerSerGluAsp 140
Db 393 CAAGTTCCTGTGCTCGCTCGTGGAAACAAAGATTATCCGTCACGCTTCTTCTGAAAGAC 452
Qy 141 GluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyYsGlyThrValAsnLeuGly 160
Db 453 GAGTTGGGTTCAACCTTGGTTGACATGACCATGCTGTAAAGAAACGGTGAACCTGGGA 512
Qy 161 AspSerAsnIleArgProIleGluValPheMetCysSerIleValArgYsMetGlyTyr 180
Db 513 GATAGCAACATTCGGCCCATGAGGTTTTCATGTGCAATATTGTGGCAAAATGGGGTAC 572
Qy 181 GlyGluGlyPheIlySTPMeThrGlnTyrIleYs 192
Db 573 GGTGAAGGTTCAAGTGATGACCCAGTACATCAAG 608

RESULT 2
LOCUS AX282608 667 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 6 from Patent WO0177161.
ACCESSION AX282608
VERSION AX282608.1 GI:16609685
KEYWORDS
SOURCE Physcomitrella patens
ORGANISM Physcomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
REFERENCE 1
AUTHORS da Costa e Silva,O., Bohner,H.J., van Thiel,N., and Chen,R.
TITLE Gtp binding stress-related proteins and methods of use in plants
JOURNAL Patent: WO 0177161-A 6 18-OCT-2001;
BASF Plant Science GmbH (DE)
FEATURES
source location/Qualifiers
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/organism="Physcomitrella patens"
/mol_type="unassigned DNA"
/db_xref="taxon:3218"

ORIGIN
Alignment Scores: 1.14e-96 Length: 667
Pred. No.: 998.00 Matches: 192
Score: 998.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-688-481-11 (1-192) x AX282608 (1-667)

Qy 1 MetPheLeuValAspTTPPhetYrGlyPheLeuAlaSerIleGlyLeuTPGlnLyGlu 20
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Qy 21 AlAlaYsIleLeuPheLeuGlyLeuAspAsnAlaGlyYsThrThrLeuLeuHisMetLeu 40
Db 93 GCCAAATCCTGTTCTGGCTCGACAAATCTGGCAAGACTACTCTTTCGACATGCTC 152
Qy 41 LysAspGluYsLeuGlyGlnHisGlnProThrGlnTyrProThrsSerGluLeuSer 60
Db 153 AAGGATGAGAACTGGGGCAACATCAACCAACGAGATCAACGTCAGAGAGTTGAGT 212
Qy 61 IleAsnArgValIlyPheYsAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db 213 ATCAACAGAGTGAAGTTCMAAGCATTCGATCTGGTGGCCACAAATCGCTCGACGGTG 272
Qy 81 TrpArgAspTyrTyrAlaYsValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db 273 TGGAGGACTACTATGCTTAAGTGATGCTATAGTATCTCGTCGACGACGTAGACAG 332
Qy 101 GluArgPheAlaGluSerIlyYsGluLeuAspSerLeuSerAspAspSerLeuSer 120
Db 333 GAGAGATTGCTGATCAAGAAAGAGCTCGATTCCTCTCTCCGACGATTCCTGTCC 392
Qy 121 GlnValProValLeuValLeuGlyYsAsnYsIleAspIleProTyrAlaSerSerGluAsp 140
Db 393 CAAGTTCCTGTGCTCGCTCGTGGAAACAAAGATTATCCGTCACGCTTCTTCTGAAAGAC 452
Qy 141 GluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyYsGlyThrValAsnLeuGly 160
Db 453 GAGTTGGGTTCAACCTTGGTTGACATGACCATGCTGTAAAGAAACGGTGAACCTGGGA 512
Qy 161 AspSerAsnIleArgProIleGluValPheMetCysSerIleValArgYsMetGlyTyr 180
Db 513 GATAGCAACATTCGGCCCATGAGGTTTTCATGTGCAATATTGTGGCAAAATGGGGTAC 572
Qy 181 GlyGluGlyPheIlySTPMeThrGlnTyrIleYs 192
Db 573 GGTGAAGGTTCAAGTGATGACCCAGTACATCAAG 608

RESULT 3
LOCUS AR474304/c 805 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1 from patent US 6689399.
ACCESSION AR474304
VERSION AR474304.1 GI:42713152
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 805)
AUTHORS da Costa e Silva,O., Bohner,H.J., van Thiel,N., and Chen,R.
TITLE GTP binding stress-related proteins and methods of use in plants
JOURNAL Patent: US 6689399-A 1 10-FEB-2004;
BASF Plant Science GmbH; Ludwigshafen;
WOX;
FEATURES
source location/Qualifiers
1..805
/organism="unknown"
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ORIGIN
Alignment Scores: 1.43e-96 Length: 805
Pred. No.: 998.00 Matches: 192
Score: 998.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0
US-10-688-481-11 (1-192) x AR474304 (1-805)
QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnIlybGlu 20
Db 753 ATGTTCTTGATGATTGGTTTACGGCTTCTTGCGAGCATAGGGCTGTGGCAAGAGAG 694
QY 21 AlaIlyIleLeuPheLeuGlyLeuAspAsnAlaGlyIlySerThrThrLeuLeuHismetLeu 40
Db 693 GCCAAATCTGTTTCTGGGCTCGAATGCTGGCAAGACTACTCTTCTGCAATGCTC 634
QY 41 LysAspGlnIlybLeuGlyGlnHisGlnProThrGlnTyrProThrSerGlnIlyLeuSer 60
Db 633 AAGGATGAGAACTGGGGCAATCAACCAAGCATCAACGTCAGAGGTTGAGT 574
QY 61 IleAsnArgValIlybPheIlybAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db 573 ATCAACAGATGAGATTCAAGCATTCGATCTGGGTGGCCACAAATCGCTCGACCGGTG 514
QY 81 TrpArgAspTyrTyrAlaIlybValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db 513 TGGAGGACTACTATGCTAAAGTGATGCTATAGTATCTCGTCAAGCATGAGACAG 454
QY 101 GluArgPheAlaGlnSerIlybIlybGlnLeuAspSerLeuSerAspAspSerLeuSer 120
Db 453 GAGAGATTGCTGATGCAAAAGAAAGCTGATTTCTTCTCTCGACGATCTCTGTCC 394
QY 121 GlnValProValIleuValIleuGlyAsnIlybIleAspIleProTyrAlaSerSerGluAsp 140
Db 393 CAAGTCTGTGCTCGTCTGGGAAACAAAGATTGATCCGATCGCTTCTTGAAGAC 334
QY 141 GlnLeuArgPheThrLeuGlyLeuThrMetThrThrGlyIlybGlyThrValAsnLeuGly 160
Db 333 GAGTTGGGTTCACACTTGGGTGACCATGACCTGTAAAGAAAGGTAACCTGGGA 274
QY 161 AspSerAsnIleArgProIleGlnValPheMetCysSerIleValArgIlybMetGlyTyr 180
Db 273 GATGCAACATTGCGCCCATTTGAGTTTTCATGTGCGATTGTGGCCAAATGGGGTAC 214
QY 181 GlyGlnGlyPheIlybTrpMetThrGlnTyrIleIys 192
Db 213 GGTGAAGTTTCAAGTGATGACCACTGATCAAG 178
RESULT 4
LOCUS AX282603 805 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 1 from Patent WO0177161.
ACCESSION AX282603
VERSION AX282603.1 GI:16609680
KEYWORDS
SOURCE Physcomitrella patens
ORGANISM Physcomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariaceae; Funariales; Funariaceae; Physcomitrella.
REFERENCE 1 da Costa e Silva, O., Bohmert, H.U., van Thiel, N. and Chen, R.
AUTHORS GTP binding stress-related proteins and methods of use in plants
TITLE Patent: WO 0177161-A 1 18-Oct-2001;
JOURNAL BASF Plant Science GmbH (DE)
FEATURES
source location/Qualifiers
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/organism="Physcomitrella patens"
/mol_type="unassigned DNA"
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Alignment Scores: 1.43e-96 Length: 805
Pred. No.: 998.00 Matches: 192
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00%

DB: 6 Gaps: 0
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Db 753 ATGTTCTTGATGATTGGTTTACGGCTTCTTGCGAGCATAGGGCTGTGGCAAGAGAG 694
QY 21 AlaIlyIleLeuPheLeuGlyLeuAspAsnAlaGlyIlySerThrThrLeuLeuHismetLeu 40
Db 693 GCCAAATCTGTTTCTGGGCTCGAATGCTGGCAAGACTACTCTTCTGCAATGCTC 634
QY 41 LysAspGlnIlybLeuGlyGlnHisGlnProThrGlnTyrProThrSerGlnIlyLeuSer 60
Db 633 AAGGATGAGAACTGGGGCAATCAACCAAGCATCAACGTCAGAGGTTGAGT 574
QY 61 IleAsnArgValIlybPheIlybAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db 573 ATCAACAGATGAGATTCAAGCATTCGATCTGGGTGGCCACAAATCGCTCGACCGGTG 514
QY 81 TrpArgAspTyrTyrAlaIlybValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db 513 TGGAGGACTACTATGCTAAAGTGATGCTATAGTATCTCGTCAAGCATGAGACAG 454
QY 101 GluArgPheAlaGlnSerIlybIlybGlnLeuAspSerLeuSerAspAspSerLeuSer 120
Db 453 GAGAGATTGCTGATGCAAAAGAAAGCTGATTTCTTCTCTCGACGATCTCTGTCC 394
QY 121 GlnValProValIleuValIleuGlyAsnIlybIleAspIleProTyrAlaSerSerGluAsp 140
Db 393 CAAGTCTGTGCTCGTCTGGGAAACAAAGATTGATCCGATCGCTTCTTGAAGAC 334
QY 141 GlnLeuArgPheThrLeuGlyLeuThrMetThrThrGlyIlybGlyThrValAsnLeuGly 160
Db 333 GAGTTGGGTTCACACTTGGGTGACCATGACCTGTAAAGAAAGGTAACCTGGGA 274
QY 161 AspSerAsnIleArgProIleGlnValPheMetCysSerIleValArgIlybMetGlyTyr 180
Db 273 GATGCAACATTGCGCCCATTTGAGTTTTCATGTGCGATTGTGGCCAAATGGGGTAC 214
QY 181 GlyGlnGlyPheIlybTrpMetThrGlnTyrIleIys 192
Db 213 GGTGAAGTTTCAAGTGATGACCACTGATCAAG 178
RESULT 5
LOCUS AY596178 945 bp mRNA linear PLN 08-MAY-2004
DEFINITION Zea mays putative ras-1-like small GTP binding protein mRNA, complete
cds.
ACCESSION AY596178
VERSION AY596178.1 GI:46946655
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 Zhang, Z., Tang, W. and Zheng, Y.
AUTHORS Suppressing apoptosis is a key mechanism of maize S-CMS restore
TITLE gene Rf3
JOURNAL unpublished
REFERENCE 2 (bases 1 to 945)
AUTHORS Zhang, Z., Tang, W. and Zheng, Y.
TITLE Direct Submission
JOURNAL Submitted (11-APR-2004) National Key Lab of Crop Genetic
Improvement, Huangzhong Agricultural University, Wuhan, Hubei
430070, China
FEATURES
source location/Qualifiers
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/mol_type="mRNA"
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/protein_id="AA06576.1"
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/translation="MPLVDWVGVTASGLIMQEKATILFLGLDNAGKTTLLMLKDER
LVHQHPQVPTSEELSGIRIKFKAFDGLGQHIARWMDYAKDAVVLVDAYDKER
PAEKSLDALDLADDSLANVPEFLIKNDIKPYAASEELRYLGLSNFTTGKNVNL
ADSNVRPELKIIMCSVVRKMGYGEQFKMSYIK"

ORIGIN

Alignment Scores:
Pred. No.: 1,46e-83 Length: 945
Score: 876.50 Matches: 162
Percent Similarity: 94.30% Conservative: 20
Best Local Similarity: 83.94% Mismatches: 10
Query Match: 87.83% Indels: 1
DB: Gaps: 1

US-10-688-481-11 (1-192) x AY596178 (1-945)

Oy 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnLysGln 20
Db 71 ATGTTCCGTGGTGAAGTGGTCTTATGAGGGGTGGCGGATCGTTGGGCTGTGGCAGAGAG 130

Oy 21 AAlaYsIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHisLeu 40
Db 131 GCTAAGATCCCTCTCTCTGGGCTCCACAAAGCCGGCAAGACACCCTCTTCCATGCTG 190

Oy 41 LysAspGluLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluLeuSer 60
Db 191 AAGGACGAGCGGCTGTACAGACACCGGACGAGTACCCGACCTCGAAGAGTTGAGC 250

Oy 61 ILLeaAspValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db 251 ATCGGCAGATCAAGTCAAGGCGTTGATGCTGTGCTAGTGGGCGGCACAGATGCCCGCGCT 310

Oy 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db 311 TGGAAAGACTACTACGCCAAGGTTGATGCTGTGCTAGTGGTGGTGGTGGTGGTGGTGGT 370

Oy 101 GlnArgPheAlaGlnSerLysLysGluLeuAspSerIleLeuSerAspAspSerLeuSer 120
Db 371 GAACGTTTGGCGAAGTCCAGAAAGAGGCTTGATGGCTTTCGACGATGACTCCCTTGCA 430

Oy 121 GlnValProValLeuValLeuGlyLysAspIleAspIleProTyrAlaSerSerGluAsp 140
Db 431 AACGTTCTTCTTCATACTATCGGCAACAAGATTGATCCATCCATGCGGCTTCAAGAGAG 490

Oy 141 GluLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyLysGlyThrValAsnLeu 159
Db 491 GAGCTGAAGTACTACTCGGCTCGGCTGAGCAACTCAACACGGGAAAGGCAACGTGAACCTTG 550

Oy 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValAlaGlyMetGly 179
Db 551 GCCGACTCCAAAGTCCGGCGCCCTGGAAGATCTTCATGTCAGTGTGTGTGGCAGATGGCG 610

Oy 180 TyrGlyGlnGlyPheLysTrpMetThrGlnTyrIleLys 192
Db 611 TATGGCGAAGGCTCAAAATGATGATGTCATGATCAATCAAG 649

RESULT 6
AKI11979 1035 bp mRNA linear PLN 29-OCT-2003
LOCUS Oryza sativa (japonica cultivar-group) cDNA clone:001-008-G03, full
DEFINITION
insert sequence.
ACCESSION AKI11979
VERSION AKI11979.1 GI:37986642
KEYWORDS FLI CDNA; oligo capping.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group); Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta;

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REFERENCE	TITLE
1	<p>Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.</p> <p>The Rice Full-length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA Project Team, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yasaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group, Otsu, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurotsaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN: Kawai, J., Gernicini, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kigawa, I., Kondo, S., Kono, H., Miyazaki, A., Otsu, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.</p> <p>Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice</p> <p>Science 301 (5631), 376-379 (2003)</p> <p>12869764</p>
2	<p>Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashizaki, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kigawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Kurotsaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murakami, M., Nagata, T., Nakahama, Y., Nakamura, M., Namiki, T., Narikawa, R., Nishikura, J., Nishii, K., Nomura, K., Numasaki, R., Ohneda, E., Ohta, M., Ohtsuki, K., Oka, M., Ooka, H., Otsu, N., Ota, Y., Otsu, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaki-Akahita, S., Tanaka, T., Tomaru, A., Toyota, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yasaki, J., Yokomizo, S., and Yoshimura, A.</p> <p>Rice full-length cDNA</p> <p>Unpublished</p> <p>3 (bases 1 to 1035)</p>
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Yanamoto, M. and Nakahama, Y.,
 FALS Genome Sequencing & Analysis Group: Otsu, Y., Iida, Y.,
 Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M.,
 Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M.,
 Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nikura, J., Oka, M.,
 Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsumoda, Y., Ueda, M.,
 Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.,
 Genome Exploration Research Group in Riken Genomic Sciences Center
 and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
 Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
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 Tagami-Takeda, Y., Tagawa, A., Takehashi, F.,
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FEATURES

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 /cultivar="Nipponbare"
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ORIGIN

Alignment Scores:
 Pred. No.: 4,34e-83 Length: 1035
 Score: 872.50 Matches: 161
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 Best Local Similarity: 83.42% Mismatch: 11
 Query Match: 87.42% Indels: 1
 DB: 15 Gaps: 1

US-10-688-481-11 (1-192) x AK119548 (1-1035)

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 150 GCCAAGATCTCTTCTCTGGCTCGACCAACGCCGCAAGACCACTCTCTCACAATGCTC 209
 41 LysAspGlnuLeuLeuGlyGlnHieGlnProThrGlnTyProThrSerGluGluLeuSer 60
 210 AAGCAGCAGCGGCTGTGTGACGACGACGCGAGCGAGTACCGACGTCGAGAGAGCTGAGC 269
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 330 TGGAAAGCATCTACTACGCCAAGCTCATCTGTCTTTTACTTGTGTGAGTCCCGCTGACAGA 389
 101 GluArgPheAlaGluSerIleValGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
 390 GAACGGTTTGGCGAGTCAAGAAAGAAAGCACTCGATGCCCTTCCTTGACAGCATCTCCCTACCA 449
 121 GlnValProValLeuValLeuGlyValAsnTyIleAspIleProTyAlaIleSerSerGluAsp 140
 450 ACCGGGCTTTCCTTCTACTGTGGAAACAAGATGACATCCCATACGCGCGCTGGAGAG 509
 141 GluLeuArgPheThrLeuGlyLeuThr---MetTrpThrGlyTyLeuGlyThrValAsnLeu 159
 510 GAATCTCCGCTACTACTTGTGCTGTGAGCAACTTACCAACCGGTAAAGGCAAGTGAACCTTA 569

Oy 160 GlyAspSerAsnIleLeuArgProIleGluValPheMetCysSerIleValArgLeuMetGly 179
 Db 570 GCCGATCCCAACGTGGCGCTCTGAGATCTTATGTGACGCGCTGTCCGAAAGATGGC 629
 Oy 180 TyGlyGluGlyPheLeuTrpMetThrGlnTyIleLeu 192
 Db 630 TACGGCAAGCTTCAATGATGATGTCCTCATCATCAA 668

RESULT 8
 AK11904
 LOCUS
 DEFINITION
 Oryza sativa (japonica cultivar-group) cDNA clone:J023112F13, full
 insert sequence.

ACCESSION
 AK11904
 VERSION
 AK11904.1 GI:37988567
 FLI CDNA; CAP trapper.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 ORGANISM
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 The Rice Full-length cDNA Consortium, National Institute of
 Agrobiological Sciences Rice Full-length cDNA Project Team,
 Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
 Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
 Kojima, K., Nami, K., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
 Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
 Science Genome Sequencing & Analysis Group: Otsu, Y., Murakami, K.,
 Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsumoda, Y.,
 Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
 Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nikura, J.,
 Ikeda, R., Ishibiki, J., Kawamata, M., Matsubara, K., RIKEN:
 Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsumura, A., Miura, J.,
 Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
 Hara, A., Hashizume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
 Kagawa, I., Kondo, S., Kono, H., Miyazaki, A., Oosato, N., Ota, Y.,
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 Yoshino, M. and Hayashizaki, Y.

TITLE

Collection, mapping, and annotation of over 28,000 cDNA clones from
 japonica rice
 Science 301 (5631), 376-379 (2003)

JOURNAL

12869764

PUBMED

12869764

REFERENCE

12869764

AUTHORS

12869764

TITLE

Rice full-length cDNA

JOURNAL

Unpublished

PUBMED

Unpublished

REFERENCE

Unpublished

AUTHORS

Unpublished

TITLE

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JOURNAL

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REFERENCE

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Qy 1 MetPheLeuValAspTrpPheTyrglyPheLeuAlaSerilegIleuTrpGlnlyGlu 20
Db 57 ATGTTCTGCTGAGTGGTCTTACGGGGTGTGGCTCTGGGGCTGTGGCAGAAAGAG 116
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Qy 41 LysAspGlyIleuGlyGlnHImeGlnProThrGlnTyrglyProThrSerGlnIleuSer 60
Db 177 AAGACCGAGCGGCTCTGTCAGACACCGACGACGACGACGACGACGACGACGACGAC 236
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Db 237 ATCCGCAAGATCAAGTTCAGAGCTTCGACCTCGCGCGCCACAGATCGCGCGCGCTC 296
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Qy 101 GluArgPheAlaGlySerIleGlyIleuAspSerIleuSerAspAspSerIleuSer 120
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Qy 121 GlnValProValIleuValIleuGlyAsnIleAspIleProTyrglyAspSerGluasp 140
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Qy 160 GlyAspSerAnaIleArgProIleGlnValPheMetCysSerIleValArgIleMetGly 179
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Qy 180 TyrglyGlnGlyPheIleTyrglyMetThrGlnTyrglyIleIys 192
Db 597 TACGGCGAAGGCTCAATGATGTCGACATCAATCAAA 635
RESULT 10
AF210431 582 bp mRNA linear PLN 13-DEC-1999
LOCUS Nicotiana tabacum small GTP-binding protein Sar1BNC mRNA, complete
DEFINITION cds.
ACCESSION AF210431
VERSION AF210431.1 GI:6563321
KEYWORDS
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Solanales; Solanaceae; Nicotiana.
REFERENCE
1 (bases 1 to 582)
Andreeva,A.V., Kutzov,M.A., Evans,D.E. and Hawes,C.R.
Plant proteins involved in membrane transport between the
endoplasmic reticulum and the Golgi apparatus
Unpublished
JOURNAL
REFERENCE
TITLE 2 (bases 1 to 582)
AUTHORS Andreeva,A.V.
DIRECT SUBMISSION
SUBMITTED (02-DEC-1999) Reseach School of Biological and Molecular
Sciences, Oxford Brookes University, Gipsy lane, Oxford, Oxon OX3
0BP, U.K.
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Pred. No.: 2,76e-83 Length: 582
Score: 871.50 Matches: 161
Percent Similarity: 94.30% Conservative: 21
Best Local Similarity: 83.42% Mismatches: 10
Query Match: 87.32% Indels: 1
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US-10-688-481-11 (1-192) x AF210431 (1-582)
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Qy 21 AAlaValIleuPheLeuGlyIleuAspAnaIaGlyThrThrIleuLeuHImeLeu 40
Db 61 GCTAAGATCTGTTGTTTGGGCTCTGATAATCGGCAAAACCACTTGCTTCATATGTTG 120
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DEFINITION
ACCESSION L12051
VERSION L12051.1 GI:473683
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ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE
1 (bases 1 to 957)
Davies,C.
Cloning and characterization of a tomato GTPase-like gene related

to Yeast and Arabidopsis genes involved in vesicular transport
Plant Mol. Biol. 24 (3), 525-531 (1994)

JOURNAL

PUBMED

8123194

COMMENT Original source text: Lycopersicon esculentum (library: lambda
gt11) immature green pericarp cDNA to mRNA.

FEATURES

source

Location/Qualifiers

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ORIGIN

3' UTR

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Query Match:	86.42%	Indels:	1
DB:	15	Gaps:	1

US-10-688-481-11 (1-192) x AY096699 (1-613)

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Db 1 ATGTTTCATGATCGATGTTGTTCTATGGCGTTCTCCCTTCGTTAGCGTTATGCGCAAAAGAG 60
Qy 21 AAlaLyS1leLeuPheLeuGlyLeuAspAsnAlaGlyLyThrThrLeuLeuH1MetLeu 40
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RESULT 13
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DEFINITION Arabidopsis thaliana clone 94610 mRNA, complete sequence.
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VERSION AY088765.1 GI:21407539
KEYWORDS FLI CDNA.
SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

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REFERENCE

1 (base 1 to 884)
Haas,B.O., Volkovskiy,N., Town,C.D., Troukhan,M., Alexandrov,N.,
Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
Full-length messenger RNA sequences greatly improve genome
annotation
Genome Biol. 3 (6), RESEARCH0029 (2002)
12093376

2 (bases 1 to 884)
Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Full-length cDNA from Arabidopsis thaliana
Unpublished
3 (bases 1 to 884)
Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Direct Submission
Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
Malibu, CA 90265, USA

TITLE

JOURNAL

REFERENCE

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FEATURES

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CDS

ORIGIN

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US-10-688-481-11 (1-192) x AY088765 (1-884)

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RESULT 14
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DEFINITION Arabidopsis thaliana GTP binding protein, Sar1 homolog (ASAR1)
ACCESSION U56929
VERSION U56929.1 GI:1314859
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE 1. Winge, P., Brembu, T., and Bones, A.M.
AUTHORS The Arabidopsis thaliana Sar-like genes belongs to a multigene
TITLE family
JOURNAL Unpublished (1996)
AUTHORS 2. (bases 1 to 899)
Winge, P., Brembu, T., and Bones, A.M.
DIRECT SUBMISSION Submitted (26-APR-1996) Per Winge, UNIGEN, MTFIS, University of
JOURNAL Trondheim, Olav Kyrresgaat 3, Trondheim N7005, Norway
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DB: 15 Gaps: 1

US-10-688-481-11 (1-192) x ATU56929 (1-899)
QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnIleGly 20
Db 71 ATGTTCAATATGATGATTTGTTATGCGCTTCTGCTGTTAGGCTTATGGAGAAAG 130
QY 21 AlaIleLeuPheLeuGlyLeuAspAlaGlyIleThrIleLeuLeuHisMetLeu 40
Db 131 GCTAAGATCTTGTCTTCTGGAATGCTGATTAATGCTGTAACCACTGCTTCAATGTTG 190
QY 41 LysAspGluValLeuGlyGlnHisGlnProThrGlnTyr-ProThrSerGlnGluLeuSer 60
Db 191 AAAGAGAGAGATGGTATACGATCAGCCATGACGACATCAACTTGTGAAGAATCAGC 250
QY 61 IleAsnArgValIlePheLeuValIlePheAspLeuGlyGlyHisThrIleAlaArgArgVal 80
Db 251 ATGGGAAATCAAGTTTAAAGCTTTTGAATTTGGTGTGTACCAAGATGCTGCAGAGGTC 310
QY 81 TrpArgAspTyrTyrIleAlaValIleAspIleProTyrIleAspSerGluAsp 100
Db 311 TGGAGATTAATCAATCTAAGGAGGAGCGTGTGTCTTACCTAAGTTATGCTTACGACAA 370
QY 101 GluArgPheAlaGluSerIleGlyGluLeuAspSerIleLeuSerAspAspSerLeuSer 120
Db 371 GAGAGATTGCAAGATCAAAAAAGAACTTGATGACCTTCTTCACAGCAATCCCTAGCC 430
QY 121 GlnValProValIleValLeuGlyAsnIleAspIleProTyrIleAspSerGluAsp 140
Db 431 AGCGTTCATCTCTCAATCTTAGAAGAAACAGATAGACATACCGATCTGCATCAGAGAC 490
QY 141 GluLeuArgPheThrIleGlyLeuThr--MetThrThrGlyGlyGlyThrValIleLeu 159
Db 491 GAGCTCCGTTACATCTCGGCTCTCCAACTTCACTACAGAAAGGTAAGGAAATCTA 550
QY 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValAlaArgIleMetGly 179
Db 551 ACGGATTCAGACGTTAGCGCATGAGGATTTTATGTGACGATTTGTGAGAAATGGGT 610
QY 180 TyrGlyGluGlyPheLeuTyrMetThrGlnTyrIleLeu 192
Db 611 TACGAGAAAGCTTCAAAATGGGTTTTCATATCATCAATCAAG 649

RESULT 15
LOCUS AY065357 926 bp mRNA linear PLN 18-SEP-2002
DEFINITION Arabidopsis thaliana putative SAR1/GTP-binding secretory factor
ACCESSION AY065357
VERSION AY065357.1 GI:17529143
KEYWORDS FLI CDNA.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE 1. Winge, P., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K.,
AUTHORS Yamada, K.,

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OW protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 01:38:02 ; Search time 469 Seconds
(without alignments)
2728.403 Million cell updates/sec

Title: US-10-688-481-11
Perfect score: 998
Sequence: 1 MFVLDVFGYGLASIGLWQKE.....SIVRKKGYGEGFKMTQYIK 192

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seque, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
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-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: geneseqn1990s: *
3: geneseqn2000s: *
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10: geneseqn2003cs: *
11: geneseqn2003ds: *
12: geneseqn2004as: *
13: geneseqn2004bs: *
14: geneseqn2005s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	998	100.0	667	6	ABN89814 Physcomit
2	998	100.0	667	13	ADT91569 Physcomit
3	998	100.0	805	6	ABN89809 Physcomit
4	998	100.0	805	13	ADT91564 Physcomit

5	880.5	88.2	955	13	ADx46899 plant ful
6	880.5	88.2	966	13	ADx30716 plant ful
7	880.5	88.2	1017	13	ADx62537 plant ful
8	871.5	87.3	811	11	ADm45502 insect re
9	871.5	87.3	830	11	ADm45760 insect re
10	867.5	86.9	1164	13	ADx52065 plant ful
11	865.5	86.7	615	11	ADm45777 insect re
12	864.5	86.6	1047	13	ADr60523 cotton cd
13	862.5	86.4	876	11	AC134445 rice abio
14	862.5	86.4	885	3	AAc23538 Arabidops
15	862.5	86.4	928	6	ABK71577 Human dit
16	862.5	86.4	966	13	ADx45605 plant ful
17	862.5	86.4	998	13	ADx12667 plant ful
18	862.5	86.4	1051	13	ADx45551 plant ful
19	862.5	86.4	1073	13	ADm81658 plant ful
20	862.5	86.4	1117	13	ADx52362 plant ful
21	860.5	86.2	952	14	ABE67368 Rice geno
22	859.5	86.1	608	9	AC118989 DNA clone
23	859.5	86.1	928	13	ADx29066 plant ful
24	853.5	85.5	807	13	ADr60521 cotton cd
25	852.5	85.4	582	7	ADZ75277 Rice ORF
26	850.5	85.2	904	3	AAc36976 Arabidops
27	848.5	85.0	1233	3	AAc44481 Zea maye
28	842.5	84.4	994	13	ADr60522 cotton cd
29	823.5	82.5	675	6	ABO65802 Arabidops
30	822.5	82.4	582	3	AAc42867 Arabidops
31	820.5	82.2	834	7	ADZ75292 Rice ORF
32	815.5	81.7	592	13	ACN60391 cotton gy
33	793	79.5	1102	11	AC132345 Rice abio
34	792.5	79.4	640	11	ADm44923 insect re
35	792.5	79.4	669	11	ADm45787 insect re
36	792.5	79.4	669	11	ADm45518 insect re
37	791	79.3	680	11	ADm44921 insect re
38	791	79.3	689	11	ADm45514 insect re
39	791	79.3	689	11	ADm45782 insect re
40	742.5	74.4	657	7	ADZ75275 Rice ORF
41	729.5	73.1	695	9	AC118994 DNA clone
42	728.5	73.0	594	7	ADZ74937 cotton pr
43	725.5	72.7	569	13	ACN48893 Arabidops
44	725.5	72.7	580	11	ADm45500 insect re
45	718.5	72.0	715	11	ADm45798 insect re

ALIGNMENTS

RESULT 1
ID ABN89814 standard; cDNA; 667 BP.
XX
AC ABN89814;
XX
DT 18-SEP-2002 (first entry)
XX
DE Physcomitrella patens GBP-1 encoding cDNA sequence SEQ ID NO:6.
XX
KW Physcomitrella patens; GBP; GTP binding protein; GBSRP; plant;
KW GTP binding stress-related protein; transgenic plant; agricultural;
KW environmental stress; salinity; drought; temperature; gene; ss.
XX
OS Physcomitrella patens.
XX
FH Key Location/Qualifiers
FT CDS 33..611
FT /*tag= a
FT /product= "GTP-binding protein 1 (GBP-1)"
XX
PN US2002066124-A1.
XX
PD 30-MAY-2002.
XX
PF 06-APR-2001; 2001US-00828310.
XX
PR 07-APR-2000; 2000US-0196001P.

XX (SILV/) SILVA O D C E.
 PA (BOHN/) BOHNERT H J.
 PA (THIE/) THIELEN N V.
 PA (CHEN/) CHEN R.
 XX
 PI Silva ODCE, Bohnert HJ, Thielen NV, Chen R;
 XX
 DR WPI: 2002-556781/59.
 P-PSDB: ABB81583.
 XX
 PT Novel GTP binding stress-related proteins and genes encoding the
 PT proteins, useful for producing transgenic plants having increased
 PT tolerance to environmental stress as compared to wild type variety of
 PT plant cell.
 XX
 PS Claim 16; Fig 2A; 73pp; English.

XX The present invention describes an isolated GTP binding stress-related
 CC protein (GBSRP) (I) from Physcomitrella patens, selected from GTP binding
 CC protein-1 (GBP-1), GBP-2, GBP-3, GBP-4 and GBP-5, or its orthologues. (I)
 CC can be used for producing a transgenic plant (e.g. maize, wheat, rye,
 CC oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola,
 CC manihot, pepper, sunflower, tagetes, solanaceous plants, potato, tobacco,
 CC eggplant, tomato, Vicia species, pea, alfalfa, coffee, cacao, tea, Salix
 CC species, oil palm, coconut, perennial grass and forage crops). The
 CC transgenic plants produced have increased tolerance to environmental
 CC stress (e.g. salinity, drought and temperature) as compared to a wild
 CC type variety of the plant, from the plant cell. GBSRP polynucleotide
 CC sequences can be used as markers for specific regions of the genome, and
 CC also in functional studies of P. patens proteins. They can also be used
 CC for evolutionary and protein structural studies. The present sequence
 CC encodes the P. patens GBP-1 protein, which is used in the exemplification
 CC of the present invention

XX Sequence 667 BP; 169 A; 142 C; 185 G; 171 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,3e-117 Length: 667
 Score: 998.00 Matches: 192
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0

US-10-688-481-11 (1-192) X ABB89814 (1-667)

QY 1 MetPheIeuValAapTPPheTYGlyPheLeuAlaSerIleGlyLeuTyrGlnLysGlu 20
 Db 33 ATGTTCTTGTAGATTGGTTTACGGCTTTCTTCGAGCATAGGGCTGTGCAGAGAGAG 92
 QY 21 AAlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrIleuLeuMetLeu 40
 Db 93 GCCAAATCTGTTCTGGGTCGACATCTGGCAAGACTGACTCTTTCACATGCTC 152
 QY 41 LysAspGlnLysLeuGlyGlnHISGlnProThrGlnTyrProThrSerGlnLysSer 60
 Db 153 AAGGATGAGAAACGGGGCAACATCAACAGCGATTCACAGTGCAGAGAGTTGAGT 212
 QY 61 ILeaAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgArgVal 80
 Db 213 ATCAACAGAGTGAAGTTCAAGCATTCGATCTGGGTGCCACACATGCTCGACGCGTG 272
 QY 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
 Db 273 TGGAGGGACTACTAGCTAAAGTGATCTAGTATTCGTCGACGACGTAGACAGG 332
 QY 101 GluArgPheAlaGluSerLysLysGlnLysAspSerLeuLeuSerAspAspSerLeuSer 120
 Db 333 GAGAGATTTCGTGAGTCAAGAAAGAGCTCGATTCTCTCTCGAGAGATTCTCTGCGC 392
 QY 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGlnAsp 140

Db 393 CAAGTTCCTGTGCTGCTCTGGAGAAACAGATTGATATCCGTAACCTTCTTGAAGAC 452
 QY 141 GluLeuArgPheThrLeuGlyLeuThrMetThrGlyLysGlyThrValAsnLeuGly 160
 Db 453 GAGTTGGGTTCCACACTTGGGTGACCATGATCAACACATGTAAGAAACGGTGAACCTGGGA 512
 QY 161 AspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGlyTyr 180
 Db 513 GATAGCAACATTCGCGCCATTGAGGTTTCATGTGCGATTTGTGGCCAAAATGGGGTAC 572
 QY 181 GlyGlnGlyPheLysThrMetThrGlnTyrIleLys 192
 Db 573 GGTAAAGTTTCAAGTGAGTACCAGTACATCAAG 608

RESULT 2

ADT91569
 ID ADT91569 standard; cDNA; 667 BP.
 AC ADT91569;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Physcomitrella patens GBP full-length cDNA, PpGBP-1.
 XX
 KM GTP-binding stress-related protein; GBSRP; transgenic plant;
 KM environmental stress tolerance; stress resistance; cell metabolism;
 KM GTP binding protein; GBP; gene; ss.
 XX
 OS Physcomitrella patens.

XX Key Location/Qualifiers
 FH CDS 33..611
 FT /*tag= a
 FT /product= "PpGBP-1 protein"

XX US2004194163-A1.

XX 30-SEP-2004.

XX 17-OCT-2003; 2003US-00688481.

XX 07-APR-2000; 2000US-0196001P.

XX 06-APR-2001; 2001US-00828310.

XX (BADI) BASF PLANT SCI GMBH.

PI Da Costa E SilvaO, Bohnert HJ, Thielen NV, Chen R;

XX WPI: 2004-698822/68.

DR P-PSDB; ADT91574.

PT Novel isolated nucleic acid encoding polypeptide e.g., GTP-binding stress
 PT related protein, useful for producing vector utilized for producing
 PT transgenic plant that has increased tolerance to environmental stress.

XX Claim 12; SEQ ID NO 6; 62pp; English.

XX The invention relates to nucleic acid sequences encoding GTP-binding
 CC stress-related proteins (GBSRP). GBSRP DNA is useful for producing a
 CC recombinant expression vector utilized for producing a transgenic plant
 CC that has increased tolerance to environmental stress, for identifying
 CC Physcomitrella patens and related organisms, for identifying and
 CC localising P. patens sequences of interest, for evolutionary studies, for
 CC determining GBSRP regions required for function, for modulating GBSRP
 CC activity, for modulating metabolism of one or more cell function, for
 CC modulating transport of one or more compounds, for modulating stress
 CC resistance or as markers for specific regions of the genome of P. patens.
 CC The present sequence is the Physcomitrella patens GTP binding protein
 CC (GBP) full-length cDNA.

XX Sequence 667 BP; 169 A; 142 C; 185 G; 171 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.3e-117 Length: 667
 Score: 998.00 Matches: 192
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-10-688-481-11 (1-192) x ADR91569 (1-667)

QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTyrGlnValGlu 20
 Db 33 ATGTTCTTGTAGATTGGTTTACGGCTTCTTCCGAGCATAGGCTGTGGCAAGAGAG 92
 QY 21 AlAlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyIleThrThrLeuLeuHISmetLeu 40
 Db 93 GCCAAATCTGTTCTGGGTCTGCAATGCTGGCAAGACTCTTCTTCCACATCTC 152
 QY 41 LysAspGluLysLeuGlyGlnHISGlnProThrGlnTyrProThrSerGluLeuSer 60
 Db 153 AAGGATGAGAACTGGGGCAACATCAACCAACGAGATCCAGTCAGAGAGTTGAGT 212
 QY 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
 Db 213 ATCAACAGAGTGAAGTTCAAAGCATTCGATCTGGTGGCCACCAATCGCTCGACGCTG 272
 QY 81 TrpArgAspTyrTrpAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
 Db 273 TGGAGGACTACTATGCTTAAGTGGATGCTATGATGATCTTCCTCGACGATGACAGG 332
 QY 101 GluArgPheAlaGluSerLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
 Db 333 GAGGATTTGCTGATCAAGAAAGAGCTGATCTTCTCTCCGACGATTCCTGTC 392
 QY 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
 Db 393 CAAGTTCCTGTGCTGCTGCTGGGAAACAGATGATATCCCGTATCTTCTGAAAGAC 452
 QY 141 GluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyGlyGlyThrValAsnLeuGly 160
 Db 453 GAGTGGCGTTCAACATTTGGGTGACCACTGGTAAAGCAAGTGAACCTGGGA 512
 QY 161 AspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGlyTyr 180
 Db 513 GATGCAACATTCGCGCCCATTTGAGTTTCATGTGCAGTATTTGGCCAAATGGGGTAC 572
 QY 181 GlyGluGlyPheLysTyrMetThrGlnTyrIleLys 192
 Db 573 GGTGAAGTTTCAAGTGAATGACCCAGTACATCAAG 608

RESULT 3

ABN89809/c
 ID ABN89809 standard; cDNA; 805 BP.

AC ABN89809;

XX 18-SEP-2002 (first entry)

XX Physcomitrella patens GBP-1 partial cDNA sequence SEQ ID NO:1.

XX Physcomitrella patens; GBP; GTP binding protein; GBSRP; plant;

XX GTP binding stress-related protein; transgenic plant; agricultural;

XX environmental stress; salinity; drought; temperature; gene; ss.

XX Physcomitrella patens.

XX US2002066124-A1.

XX 30-MAY-2002.

XX 06-APR-2001; 2001US-00828310.

XX 07-APR-2000; 2000US-0196001P.

PA (SILV/) SILVA O D C E.
 PA (BOHN/) BOHNERT H J.
 PA (THIE/) THIELEN N V.
 PA (CHEN/) CHEN R.
 PI Silva ODCE, Bohnert HJ, Thielen NV, Chen R;
 DR WPI; 2002-556781/59.
 XX

PT Novel GTP binding stress-related proteins and genes encoding the
 PT proteins, useful for producing transgenic plants having increased
 PT tolerance to environmental stress as compared to wild type variety of
 PT plant cell.

PS Example 5; Fig 1A; 73pp; English.

XX The present invention describes an isolated GTP binding stress-related
 CC protein (GBSRP) (1) from Physcomitrella patens, selected from GTP binding
 CC protein-1 (GBP-1), GBP-2, GBP-3, GBP-4 and GBP-5, or its orthologues. (1)
 CC can be used for producing a transgenic plant (e.g. maize, wheat, rye,
 CC oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola,
 CC manioc, pepper, sunflower, legumes, solanaceous plants, potato, tobacco,
 CC eggplant, tomato, Vicia species, pea, alfalfa, coffee, cacao, tea, Salix
 CC species, oil palm, coconut, perennial grass and forage crops). The
 CC transgenic plants produced have increased tolerance to environmental
 CC stress (e.g. salinity, drought and temperature) as compared to a wild
 CC type variety of the plant, from the plant cell. GBSRP polynucleotide
 CC sequences can be used as markers for specific regions of the genome, and
 CC also in functional studies of P. patens proteins. They can also be used
 CC for evolutionary and protein structural studies. The present sequence
 CC represents a P. patens GBP-1 partial cDNA sequence, which is used in the
 CC exemplification of the present invention
 XX

SQ Sequence 805 BP; 214 A; 218 C; 161 G; 212 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.7e-117 Length: 805
 Score: 998.00 Matches: 192
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-688-481-11 (1-192) x ABN89809 (1-805)

QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTyrGlnValGlu 20
 Db 753 ATGTTCTTGTAGATTGGTTTACGGCTTCTTCCGAGCATAGGCTGTGGCAAGAGAG 634
 QY 21 AlAlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyIleThrThrLeuLeuHISmetLeu 40
 Db 693 GCCAAATCTGTTCTGGGTCTGCAATGCTGGCAAGACTCTTCTTCCACATCTC 634
 QY 41 LysAspGluLysLeuGlyGlnHISGlnProThrGlnTyrProThrSerGluLeuSer 60
 Db 633 AAGGATGAGAACTGGGGCAACATCAACCAACGAGATCCAGTCAGAGAGTTGAGT 574
 QY 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
 Db 573 ATCAACAGAGTGAAGTTCAAAGCATTCGATCTGGTGGCCACCAATCGCTCGACGCTG 514
 QY 81 TrpArgAspTyrTrpAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
 Db 513 TGGAGGACTACTATGCTTAAGTGGATGCTATGATGATCTTCCTCGACGATGACAGG 454
 QY 101 GluArgPheAlaGluSerLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
 Db 453 GAGAGTTTGGTGAAGCAAGAAAGAGCTGATTCCTTCTCCGACGATTCCTGTC 394
 QY 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
 Db 393 CAAGTTCCTGTGCTGCTGCTGGGAAACAGATGATATCCCGTATCTTCTGAAAGAC 334

QY 141 GluLeuAlaArgPheThrIleuGlyLeuThrMetThrThrGlyIleGlyThrValAlaLeuGly 160
Db 333 GAGTTGGCGGTTCACTGTTGACCATGACCATGTAAGGAAACGGTGAACCTGGGA 274
QY 161 AspSerAsnIleArgProIleGluValPheMetCysSerIleValArgIleMetGlyTyr 180
Db 273 GATGACCAACATTCCGCCCATTTGAGGTTTTCATGTGAGTATTGTGCCCAAAATGGGGTAC 214
QY 181 GlyIleuGlyPheIleTyrMetThrGlnTyrIleIys 192
Db 213 GGTGAAGTTTCAAGTGATGATCAACCATGACATCAAG 178
RESULT 4
ADT91564/c
ID ADT91564 standard; cDNA; 805 BP.
XX ADT91564;
AC
XX 16-DEC-2004 (first entry)
DT
XX
XX Physcomitrella patens GBSRP EST (expression sequence tag) partial cDNA.
DE
XX GTP-binding stress-related protein; GBSRP; transgenic plant;
KM environmental stress tolerance; stress resistance; cell metabolism; EST;
KM expression sequence tag; ss.
XX
XX Physcomitrella patens.
OS
XX US2004194463-A1.
PN
XX 30-SEP-2004.
PD
XX 17-OCT-2003; 2003US-00688481.
PF
XX 07-APR-2000; 2000US-0196001P.
PR 06-APR-2001; 2001US-00828310.
XX
XX (BAD1) BASF PLANT SCI GMBH.
PA
XX Da Costa E Silveo, Bohner HJ, Thieleen NV, Chen R;
PI
XX WPI; 2004-698822/68.
DR
XX
XX Novel isolated nucleic acid encoding polypeptide e.g., GTP-binding stress
PT related protein, useful for producing vector utilized for producing
PT transgenic plant that has increased tolerance to environmental stress.
XX
XX Example 5; SEQ ID NO 1; 62pp; English.
PS
XX
XX The invention relates to nucleic acid sequences encoding GTP-binding
CC stress-related protein (GBSRP). GBSRP DNA is useful for producing a
CC recombinant expression vector utilized for producing a transgenic plant
CC that has increased tolerance to environmental stress, for identifying
CC Physcomitrella patens and related organisms, for identifying and
CC localizing P. patens sequences of interest, for evolutionary studies, for
CC determining GBSRP regions required for function, for modulating GBSRP
CC activity, for modulating metabolism of one or more cell function, for
CC modulating transport of one or more compounds, for modulating stress
CC resistance or as markers for specific regions of the genome of P. patens.
CC The present sequence is the Physcomitrella patens GBSRP EST (expression
CC sequence tag) partial cDNA.
XX
XX Sequence 805 BP; 214 A; 218 C; 161 G; 212 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1.7e-117 Length: 805
Score: 998.00 Matches: 192
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-10-688-481-11 (1-192) x ADT91564 (1-805)

QY 1 MetPheLeuValAlaPheTyrPheTyrGlyPheLeuAlaSerIleGlyLeuTyrGlnIleGly 20
Db 753 ATGTTCTTGATGATTGTTTTCACGGCTTCTTCCAGACATAGGGCTGGCGAAAGGAG 694
QY 21 AlaIleIleLeuPheIleuGlyLeuAspAsnAlaGlyIleThrThrIleuMetLeu 40
Db 693 GCCAAATCCCTGTTCTGGGCTCGACAAATGCTGGCAAGACTACTCTTCTGCACATGCTC 614
QY 41 LysAspGluIleLeuGlyGlnIleGlnProThrGlnTyrProThrSerGluIleuSer 60
Db 633 AAGCATGAGAAACTGGGGCACTCAACCAACGCAATATCAACGTCAGAGGATTGAGT 574
QY 61 IleAsnArgValIlePheIleValAlaPheAspLeuGlyIleThrIleAlaArgVal 80
Db 573 ATCAACAGAGTGAAGTCAAAAGCATTCGATCTGGGCGCACCAATCGCTCAACCGG 514
QY 81 TrpArgAspTyrTyrAlaIleValAlaPheAlaIleValTyrIleuValAspAlaIleAspArg 100
Db 513 TGGAGGACTACTATGCTAAAGTGAGTGTATGTAATCTCGACGACGATGACAG 454
QY 101 GluArgPheAlaGluSerIleValLeuValLeuGlyIleAspIleProTyrAlaSerSerGluAsp 140
Db 453 GAGGATTTGCTGAGTCAAAAGAAAGCTGATTTCTTCTCCAGCATTTCTGTGC 394
QY 121 GlnValProValIleuValIleuGlyIleAspIleProTyrAlaSerSerGluAsp 140
Db 393 CAAGTTCCTGTGCTCGTCCGCGGAAACCAAGATTGATATCCCTTCTTGAAGAC 314
QY 141 GluLeuAlaArgPheThrIleuGlyLeuThrMetThrThrGlyIleGlyThrValAlaLeuGly 160
Db 333 GAGTTGGGTTCCACACTGGGTGACCATGACCATGTAAGGAAACGGTGAACCTGGGA 274
QY 161 AspSerAsnIleArgProIleGluValPheMetCysSerIleValArgIleMetGlyTyr 180
Db 273 GATGACCAACATTCCGCCCATTTGAGGTTTTCATGTGAGTATTGTGCCCAAAATGGGGTAC 214
QY 181 GlyIleuGlyPheIleTyrMetThrGlnTyrIleIys 192
Db 213 GGTGAAGTTTCAAGTGATGATCAACCATGACATCAAG 178
RESULT 5
ADX46899
ID ADX46899 standard; cDNA; 955 BP.
XX
XX ADX46899;
AC
XX
XX 21-APR-2005 (first entry)
DT
XX
XX Plant full length insert polynucleotide seqid 21639.
DE
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
KM recombinant DNA construct; physical array; plant breeding marker;
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KM extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KM galactomanan production; lignin production; plant growth regulator;
KM yield; plant growth; plant development; seed oil; protein yield;
KM protein content; gene; ss.
XX
XX Unidentified.
OS
XX US2004034888-A1.
PN
XX
XX 19-FEB-2004.
PD
XX
XX 28-APR-2003; 2003US-00425114.
PF
XX
XX 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
XX (LIU/J.) LIU J.
PA (ZHOU/Y.) ZHOU Y.

CC recombination in plants, for improving yield by modification of
CC photoynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.

XX
SQ Sequence 966 BP; 225 A; 218 C; 294 G; 229 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,35e-102 Length: 966
Score: 880.50 Matches: 163
Percent Similarity: 94.30% Conservative: 19
Best Local Similarity: 84.46% Mismatches: 10
Query Match: 88.23% Indels: 1
DB: 13 Gaps: 1

US-10-688-481-11 (1-192) x ADX30716 (1-966)

Qy 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnIlyGlu 20
Db 130 ATGTTCTCGTGGAGCTGCTTCTATAGGGGTGCTGGCATCGCTTGGGCTGTGGCAGAGAG 189
Qy 21 AlAlaYstIleLeuPheLeuGlyLeuAspAsnAlaGlyIlyThrTrpLeuLeuHisMetLeu 40
Db 190 GCTAAGATCTCTTCTTGGCTCGACAAACCGGCAAGACACCTCTCCATCATGCTG 249
Qy 41 LysAspGluIlyLeuGlyGlnIlyGlnProThrGlnIlyProThrSerGlnLeuSer 60
Db 250 AAGAGCGAGCGGCTGTCACAGCAGCGCAGCAGTACCCCATGCTCGAAGAGTTGAGC 309
Qy 61 IleAsnArgValIlyPheLeuAlaPheAspLeuGlyIlyIlyThrIleAlaArgArgVal 80
Db 310 ATCGGACAGATCAAGATTCAAGCGCTTGCACCTTGGGCGGCAACAGATCGCCGCGCTC 369
Qy 81 TrpArgAspTrpTrpAlaIlyValAlaPheAlaIleValTyrLeuValAspAlaPheArg 100
Db 370 TGGAGGACTACTACGCAAGGTTGATCTGTGTGCTTGGTGGATGCTGTGAGCAG 429
Qy 101 GluArgPheAlaGlnSerIlyLeuGlyLeuAspSerIleLeuSerAspAspSerLeuSer 120
Db 430 GAACCTTTGGCGAATCAAGAGAGCTTGAAGCTTCTTTCAGATGACTCCCTTGCA 489
Qy 121 GlnValProValLeuValLeuGlyIlyAsnIlyIleAspIleProTyrAlaSerSerGlnAsp 140
Db 490 AACGTTCTTCTCTCATCTGGGCAACAAGATTGATCCCATCGCGGCTTCAGAGAG 549
Qy 141 GluLeuArgPheThrIleGlyIlyLeuThr--MetThrTrpGlyIlyGlyThrValAsnLeu 159
Db 550 GAGCTGAGGACTACTACCTCGGCTGGAGCAACTTCACACCGGGAAGGGCAACGTGAACCTTG 609
Qy 160 GlyAspSerAsnIleArgProIleGlnValAlaPheMetCysSerIleValArgIlyMetGly 179
Db 610 GCCGACTCATATGTCGGGCCCTCGAGATCTTCAATGTCATGTCGCGAAGATGGGC 669
Qy 180 TyrGlyGlnGlyPheLeuTrpMetThrGlnIlyIlyLeu 192
Db 670 TATGGCAAGGCTTCAAAATGATGCTCATGATCAATCAAG 708

RESULT 7
ADX62537
ID ADX62537 standard; cDNA; 1017 BP.
XX
XX ADX62537;
AC
XX 21-APR-2005 (first entry)
XX
XX Plant full length insert polynucleotide seqid 33380.
DE
XX
XX plant prosecretant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.

XX
OS Unidentified.

XX
XX US2004034888-A1.
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
XX
XX 05-NOV-2001; 2001US-00985678.
XX
XX (Liu/J.) LIU J.
XX
XX (ZHOU/J.) ZHOU Y.
XX
XX (KOVA/J.) KOVALIC D K.
XX
XX (SCRE/J.) SCREEN S E.
XX
XX (TABAS/J.) TABASKA J E.
XX
XX (CAO/Y.) CAO Y.

PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 33380; 15pp; English.

XX
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.segdata.uspco.gov/sequence.html; DocID:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for producing galactomannan,
XX lignin or plant growth regulators, for increasing the rate of homologous
XX recombination in plants, for improving yield by modification of
XX photoynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX or by providing improved plant growth and development under at least one
XX stress condition or for modifying seed oil or protein yield and/or
XX content. This sequence represents a plant full length insert
XX polynucleotide that can be used in the recombinant DNA construct of the
XX invention.

XX
SQ Sequence 1017 BP; 229 A; 229 C; 311 G; 248 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.53e-102 Length: 1017
Score: 880.50 Matches: 163
Percent Similarity: 94.30% Conservative: 19
Best Local Similarity: 84.46% Mismatches: 10
Query Match: 88.23% Indels: 1
DB: 13 Gaps: 1

US-10-688-481-11 (1-192) x ADX62537 (1-1017)

Qy 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnIlyGlu 20
Db 111 ATGTTCTCGTGGAGCTGCTTCTATAGGGGTGCTGGCATCGCTTGGGCTGTGGCAGAGAG 170
Qy 21 AlAlaYstIleLeuPheLeuGlyLeuAspAsnAlaGlyIlyThrTrpLeuLeuHisMetLeu 40
Db 171 GCTAAGATCTCTTCTTGGCTCGACAAACCGGCAAGACACCTCTCCATCATGCTG 230


```
QY 41 LysAspGluLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluLeuSer 60
D 231 AAGGACGAGGCGGCTCGTACAGCAACGACGAGTACCCAGCTCAGAAAGTTGAGC 230
QY 61 IleAsnArgValIlePheLeuGlyGlnHisGlnProThrGlnTyrProThrSer 80
D 291 ATCGGCGAGGATCAAGTTCAAGGCGTTCGACCTTGGGGGCGCACAGATCGCCCGCGTTC 350
QY 81 TrpArgAspTyrTyrIleValIleValIleValIleValIleValIleValIleVal 100
D 351 TGAAGGACGATCACTACGCGCAAGTTGATGCTGTGACTTGGGATGCTGTGACAAAG 410
QY 101 GluArgPheAlaGluSerLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
D 411 GAACGTTTCCGACGTCGAAAGAGAGCTGATCGCTTCTTCGACATGACTCCCTTGCA 470
QY 121 GlnValProValIleValIleValIleValIleValIleValIleValIleValIleVal 140
D 471 AAGCTTCTTCTTCTCATACCTGCGCAACAGATTGACATCCATACGCGGCTTCAGAGAG 530
QY 141 GluLeuArgPheThrIleuGlyLeuThr--MetThrThrGlyLysGlyThrValAsnLeu 159
D 531 GAGCTGAGTACTACCTCGGCTGAGCACTTCACACCGGAAAGGCAAGTGAACCTTG 590
QY 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGly 179
D 591 GCGGACTCCAAATGTCGCGCCCTGAGATCTTCATGTGCAAGTGTGCGCAAGATGGC 650
QY 180 TyrGlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
D 651 TATGGCGAAGGCTTCAATGATGATCTCAGTACATCAAG 689
RESULT 8
ADM45502
ID ADM45502 standard; DNA; 811 BP.
AC ADM45502;
XX
DT 03-JUN-2004 (first entry)
DE Insect resistance associated DNA sequence SegID909.
XX
XX Insect resistant phenotype; plant protectant; gene therapy;
KM Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;
KW Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.
XX
XX Unidentified.
OS
PN W02003020025-A2.
XX
PD 13-MAR-2003.
XX
PF 30-AUG-2002; 2002MO-US027882.
XX
PR 31-AUG-2001; 2001US-0316319P.
PA (DOWC ) DOW CHEM CO.
XX
PI Shukla V, Meade T, Larrinua I;
XX
DR WPI; 2003-290133/28.
PT New isolated nucleic acid having expression that results in an insect
PT resistant phenotype, useful for conferring insect resistance and for
PT producing insect-resistant plants.
XX
PS Claim 1; SEQ ID NO 909; 396pp; English.
XX
XX This invention relates to a novel isolated nucleic acid comprising, or
CC hybridising under low stringent conditions to, any of the 1214 nucleic
CC acid sequences given in the specification, where the expression of the
CC nucleic acid in a plant results in an insect resistant phenotype. The
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CC invention may be useful as a plant protectant or for gene therapy. The
CC genes are derived from Arabidopsis thaliana, Nicotiana benthamiana, Oryza
CC sativa and Papaver rhoeas. The isolated nucleic acid and vector are
CC useful for conferring insect resistance and for producing insect-
CC resistant plants. The present sequence is that of a DNA sequence of the
CC invention which may confer insect resistance to plants.
XX
SQ Sequence 811 BP; 219 A; 157 C; 199 G; 236 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 2,61e-101 Length: 811
Score: 871.50 Matches: 161
Percent Similarity: 94.30% Conservative: 21
Best Local Similarity: 83.42% Mismatches: 10
Query Match: 87.32% Indels: 1
DB: 11 Gaps: 1
US-10-688-481-11 (1-192) x ADM45502 (1-811)
QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnLysGlu 20
D 131 ATGTTCTTGTGATGATTGGTTCTATGGAATTCATGCAACGCTCGGATTTATGCGAAGAG 130
QY 21 AlaLysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHisMetLeu 40
D 191 GCTAAGATCTTGTGTTTGGGCTCGATTAATGCCGCAAAACCACTTACTCATATGTTG 250
QY 41 LysAspGluLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluLeuSer 60
D 251 AAAGATGAAGAAGATGGTTCAACATTCAGCCCAACATATCCGACGTCAGAGGAGTTAGT 310
QY 61 IleAsnArgValIlePheLeuValIlePheAspLeuGlyGlnHisGlnProThrGlnTyrProThrSer 80
D 311 ATCGCAAGATCAAGTTCAAGATTTGACTTGGGTGTCATCAAAATTGCTCGCCGTGTT 370
QY 81 TrpArgAspTyrTyrIleValIleValIleValIleValIleValIleValIleValIleVal 100
D 371 TGGAAAGATTATATATCTTAAGTCGATGCTGTGTATACTTGTGTGATTCCTTGACAA 430
QY 101 GluArgPheAlaGluSerLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
D 431 GAAAGGTTTGCAGAGGCCAAGAAAGAGCTGAGCTCTCTCTCAACGAGTCTTGCA 490
QY 121 GlnValProValIleValIleValIleValIleValIleValIleValIleValIleVal 140
D 491 ACTGTTCTTCTTCTGATACCTGGAACAGATGACATCCATATGCTGCTCAGAAAGAT 550
QY 141 GluLeuArgPheThrIleuGlyLeuThr--MetThrThrGlyLysGlyThrValAsnLeu 159
D 551 GAACGCTGTTACCATATGCGGCTACACGCGCTGACACACATGCGAAAGAAAGTAACTTG 610
QY 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGly 179
D 611 GCAGATTTCCAATGTCGCTCAGATTGAGTATTCATCTGACATAGTCCGCAAAATGGGA 670
QY 180 TyrGlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
D 671 TATGGAGAAAGGCTTCAATGATGATCTCAGTATATCAAG 709
RESULT 9
ADM45760
ID ADM45760 standard; DNA; 830 BP.
AC ADM45760;
XX
DT 03-JUN-2004 (first entry)
DE Insect resistance associated DNA sequence SegID1167.
XX
XX Insect resistant phenotype; plant protectant; gene therapy;
KM Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;
KW Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.
XX
```


OS Unidentified.
XX NC02003020025-A2.
XX
PD 13-MAR-2003.
XX
PF 30-AUG-2002; 2002W0-US027882.
XX
PR 31-AUG-2001; 2001US-0316319P.
XX
PA (DOMC) DOM CHEM CO.
XX
PI Shukla V, Meade T, Larrinua I;
XX
DR WPI; 2003-290133/28.
XX
PT New isolated nucleic acid having expression that results in an insect
PT resistant phenotype, useful for conferring insect resistance and for
PT producing insect-resistant plants.
XX
PS Claim 1; SEQ ID NO 1167; 396pp; English.
XX
CC This invention relates to a novel isolated nucleic acid comprising, or
CC hybridizing under low stringent conditions to, any of the 1214 nucleic
CC acid sequences given in the specification, where the expression of the
CC nucleic acid in a plant results in an insect resistant phenotype. The
CC invention may be useful as a plant protectant or for gene therapy. The
CC genes are derived from *Arabidopsis thaliana*, *Nicotiana benthamiana*, *Oryza
CC sativa* and *Papaver rhoeas*. The isolated nucleic acid and vector are
CC useful for conferring insect resistance and for producing insect-
CC resistant plants. The present sequence is that of a DNA sequence of the
CC invention which may confer insect resistance to plants.
XX
SQ Sequence 830 BP; 221 A; 165 C; 204 G; 240 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 2.69e-101 Length: 830
Score: 871.50 Matches: 161
Percent Similarity: 94.30% Conservative: 21
Best Local Similarity: 83.42% Mismatches: 10
Query Match: 87.32% Indels: 1
DB: 11 Gaps: 1
US-10-688-481-11 (1-192) x ADM45760 (1-830)
QY 1 MetPheLeuValaEPTpRheTyGlyPheLeuAlaSerIleGlyLeuTrGlnLysGlu 20
DB 150 ATGTTCTTGATGATGGTCTTATGGAATCTTACGCAACGCTCGGATTATGGCAGAGAG 209
QY 21 AlaLysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHISMetLeu 40
DB 210 GCTAAGATCTTGTGTTGGGCTCGATATATGCCGCAAAACACCTTACTCATATGTTG 269
QY 41 LysAspGluLysLeuGlyGlnHisGlnProThrglnTyProThrSerGlnLysSer 60
DB 270 AAAGATGAGAGATTGTTCAACATCAGCCCAACACATATCCGACGTGAGAGAGTTAGT 329
QY 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgArgAla 80
DB 330 ATCGCAAGATCTCAAGATTGACCAAGCATTTGACTGGTGTCATCAAAATGCTGCCGTGTT 389
QY 81 TrpArgAspGlyTyTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
DB 390 TGGAAAGATTATTATGCTTAAGTCAATGCTGTGTGTAATCTTGATGATTCCTTGACAAA 449
QY 101 GluArgPheAlaGluSerIleLysGlnLeuAspSerLeuLeuSerAspAspSerLeuSer 120
DB 450 GAAAGATTGCGAGATCCCAAGAAAGCTGATGCTGCTCTGCTGACGAGATCCTTGACA 509
QY 121 GlnValProValLeuValLeuGlyLysnLysIleAspIleProTyrAlaSerSerGlnAsp 140
DB 510 ACTGTTCTTCTTCTGATATCTGGGTAAACAAGATGACATCCCATATGCTGCTCAGAAAGAT 569

QY 141 GlnLeuArgPheThrLeuGlyLeuThr---MetThrThGlyLysGlyThrValaenLeu 159
DB 570 GAACGCTGTTATCCATATGGGCTTAAAGCGGCTTACCACTGGCAAAAGGTAACCTTG 629
QY 160 GlyAspSerAsnIleArgProIleGluValAPheMetCysSerIleValArgLysMetGly 179
DB 630 GCAGATTCCAAATGTCGTCACAGTTGAGTATTCATATGTCAGCATATGCTCCGCAAAATGGGA 689
QY 180 TyrGlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
DB 690 TATGAGAAAGGCTTCAGATGATGATGCTCATATATATCAAG 728
RESULT 10
ADK52065
ID ADK52065 standard; cDNA; 1164 BP.
XX
AC ADK52065;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 26805.
XX
KM plant protectant; plant growth regulator; gene therapy; plant;
KM recombinant DNA construct; physical array; plant breeding marker;
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KM extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KM galactomannan production; lignin production; plant growth regulator;
KM yield; plant growth; plant development; seed oil; protein yield;
KM protein content; gene; ss.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PD 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAO/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
DR WPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 26805; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.segdata.uspo.gov/sequence.html; DocID:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for producing galactomannan,
XX lignin or plant growth regulators, for increasing the rate of homologous
XX recombination in plants, for improving yield by modification of
XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake

CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.

XX Sequence 1164 BP; 271 A; 262 C; 361 G; 270 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,41e-100	Length:	1164
Score:	867.50	Matches:	161
Percent Similarity:	93.26%	Conservative:	19
Best Local Similarity:	83.42%	Mismatches:	12
Query Match:	86.92%	Indels:	1
DB:	13	Gaps:	1

US-10-688-481-11 (1-192) x ADM52065 (1-1164)

```
Qy 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTgTgInLysGlu 20
    |||
Db 259 ATGTTCTGCTGAGACTGCTGTTCTATGAGGCTGCTGAGCTGCTGAGCTGCTGAGAGAG 318
Qy 21 AlaLysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHisMetLeu 40
    |||
Db 319 GCTAAGATCCTCTTCTTGGCTGCTGACACGCGGCAAGACACCTCTCCACATGCTG 378
Qy 41 LysAspGluLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluGluLeuSer 60
    |||
Db 379 AAGGACGAGCGGCTCGTACGACACACCGACGACGACGACGACGACGACGACGACGACG 438
Qy 61 IleAsnArgValLysPheLysPheLysPheLysPheLysPheLysPheLysPheLysPhe 80
    |||
Db 439 ATGCGCAGATCAATCAAGGCTTCACTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 498
Qy 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
    |||
Db 499 TGGAGAGACTACTACGCGCAAGGTTGATGCTGTTGATGCTGTTGATGCTGTTGATG 558
Qy 101 GluArgPheAlaGluSerLysLysGluLeuAspSerLeuLeuSerLeuSerLeuSer 120
    |||
Db 559 GAACGTTTCCGCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 618
Qy 121 GlnValProValLeuValLeuGlyAsnLysIleLeuProTyrAlaSerSerGluAsp 140
    |||
Db 619 AACGTTCTCTTCCATACCTGCGGCAACAGATGACATCCCATACGCGGCTTCAAGAG 678
Qy 141 GluLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyLysGlyThrValAsnLeu 159
    |||
Db 679 GAGCTGAGTACCTACCTCGGCTGAGCAACTTCAACCGGGAAGGCAACGTGAATTG 738
Qy 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValLysGlyMetGly 179
    |||
Db 739 GCGGACCTCCACAGCCGCCCTCGAGATCTTCAATGCGAGTGTGCGCAAGATGCGC 798
Qy 180 TyrGlyGluGlyPheLysTyrMetThrGlnTyrIleLys 192
    |||
Db 799 TAGGCGAAGGCTTCAATGATGTCTCAAGTCAATCAAG 837

RESULT 11
ID ADM45777 standard; DNA; 615 BP.
XX
XX ADM45777;
XX
XX 03-JUN-2004 (first entry)
XX
XX Insect resistance associated DNA sequence Segid1184.
XX
XX Insect resistant phenotype; plant protectant; gene therapy;
XX Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;
XX Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.
XX
XX Unidentified.
```

XX
PN WO2003020025-A2.

XX
PD 13-MAR-2003.

XX
PF 30-AUG-2002; 2002WO-US027882.

XX
PR 31-AUG-2001; 2001US-0316319P.

XX
PA (DOWC) DOW CHEM CO.

XX
PI Shukla V, Meade T, Larrinua I;

XX
XX WPI; 2003-290133/28.

PT New isolated nucleic acid having expression that results in an insect
PT resistant phenotype, useful for conferring insect resistance and for
PT producing insect-resistant plants.

PS Claim 1; SEQ ID NO 1184; 396bp; English.

CC This invention relates to a novel isolated nucleic acid comprising, or
CC hybridizing under low stringent conditions to, any of the 1214 nucleic
CC acid sequences given in the specification, where the expression of the
CC nucleic acid in a plant results in an insect resistant phenotype. The
CC invention may be useful as a plant protectant or for gene therapy. The
CC genes are derived from Arabidopsis thaliana, Nicotiana benthamiana, Oryza
CC sativa and Papaver rhoeas. The isolated nucleic acid and vector are
CC useful for conferring insect resistance and for producing insect-
CC resistant plants. The present sequence is that of a DNA sequence of the
CC invention which may confer insect resistance to plants.

XX
SQ Sequence 615 BP; 173 A; 105 C; 167 G; 170 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.03e-100	Length:	615
Score:	865.50	Matches:	162
Percent Similarity:	92.75%	Conservative:	17
Best Local Similarity:	83.94%	Mismatches:	13
Query Match:	86.72%	Indels:	1
DB:	11	Gaps:	1

US-10-688-481-11 (1-192) x ADM45777 (1-615)

```
Qy 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTgTgInLysGlu 20
    |||
Db 29 ATGTTCTGCTGAGACTGCTGTTCTATGAGGCTGCTGAGCTGCTGAGAGAGAG 88
Qy 21 AlaLysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHisMetLeu 40
    |||
Db 89 GCGAAGTATGTTGTTTGAAGCTTGAATGCTGCGCAACCACTTGTCTTCAATGTTG 148
Qy 41 LysAspGluLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluGluLeuSer 60
    |||
Db 149 AAGAGTGAAGATTTGGTGAGCATCAACTACCAATACCAATCAATCAATCAATCAAT 208
Qy 61 IleAsnArgValLysPheLysPheLysPheLysPheLysPheLysPheLysPheLysPhe 80
    |||
Db 209 ATAGTAAATTAATTAAGTCAAGGCTTTGATTTGAGAGAGACCAAAATGCTTGAAGATC 268
Qy 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
    |||
Db 269 TGGAGAGACTACTACGCGCAAGGTTGATGCTGTTGATGCTGTTGATGCTGTTGATG 328
Qy 101 GluArgPheAlaGluSerLysLysGluLeuAspSerLeuLeuSerLeuSerLeuSer 120
    |||
Db 329 GAGAGGTTTCCGAGTCAAGAGAGAAATGAGTGGCTTCTCAGATGAGTCAATGGCA 388
Qy 121 GlnValProValLeuValLeuGlyAsnLysIleLeuProTyrAlaSerSerGluAsp 140
    |||
Db 389 AATGTCATTTCTCATCTTGGGAAACAGATGATGATATACATATGCTGCTTCAAGAGAC 448
Qy 141 GluLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyLysGlyThrValAsnLeu 159
```


|||||:::|||||:::|||||:::|||||
Db 449 GAGTCGCTATCACTTGGGCTTAAGTGTGTGACCACTGGCAAGGTAACGTAAACCTC 508
Qy 160 G[AspSer]en[le]a[ArgPro]le[glu]Val[Ph]e[Met]Cys[Ser]le[Val]a[Arg]Leu[Met]Gly 179
Db 509 GCTGCTCAAAATGTCCTCCATTCAGGTGTTATGTGCAGCATTTGTGCGCAAGATGGGA 568
Qy 180 Tyr[glu]glu[glu]Phe[leu]Tyr[Met]Thr[glu]Tyr[leu]Leu 192
Db 569 TATGTGAGGCTTCAAGTGAATGTCTCCAAATACATCAAG 607
RESULT 12
ADR60523
ID ADR60523 standard; cDNA; 1047 BP.
XX
AC ADR60523;
XX
DT 02-DEC-2004 (first entry)
XX
DE Cotton cDNA sequence, SEQ ID 1304.
XX
KW Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;
KW drought tolerance; plant disease resistance; galactomannan; lignin;
KW plant growth regulator; heat tolerance; herbicide tolerance;
KW homologous recombination; extreme osmotic condition tolerance;
KW pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
KW stress resistance.
XX
OS Gossypium hirsutum.
XX
PN US2004181830-A1.
XX
PD 16-SEP-2004.
XX
PE 29-JAN-2004; 2004US-00767795.
XX
PR 07-MAY-2001; 2001US-00849529.
PR 12-DEC-2001; 2001US-00021323.
XX
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAO/) CAO Y.
PI Kovalic DK, Zhou Y, Cao Y;
PI
XX KPI; 2004-667716/65.
DR
XX
XX
PT New recombinant nucleic acid molecules and polypeptides from Gossypium
PT hirsutum, useful for producing plants with improved biological
PT characteristics (e.g. improved plant cold or drought tolerance).
XX
PS Claim 1; SEQ ID NO 1304; 14pp; English.
XX
XX The invention relates to a recombinant polynucleotide comprising any of
CC the 58798 Cotton plant cDNA sequences mentioned in the specification.
CC Also a recombinant polypeptide comprising any of the 58798 amino acid
CC sequences mentioned in the specification and producing a plant having an
CC improved property. Producing a plant having an improved property
CC comprises transforming a plant with a recombinant construct comprising a
CC promoter region functional in a plant cell operably joined to a
CC polynucleotide comprising a coding sequence for a polypeptide associated
CC with the property, and growing the transformed plant. The polypeptide is
CC useful for improving plant cold tolerance, manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, improving plant
CC drought tolerance, providing increased resistance to plant disease,
CC producing galactomannan (or lignin or plant growth regulators), improving
CC plant heat tolerance, improving plant tolerance to herbicides, increasing
CC the rate of homologous recombination in plants, improving plant tolerance
CC to extreme osmotic conditions or to pathogens or pests, improving yield
CC by modification of photosynthesis, modifying seed oil or protein yield
CC and/or content, improving yield by modification of carbohydrate, nitrogen
CC or phosphorus use and/or uptake, or improving yield by providing improved
CC plant growth and development under at least one stress condition. The

CC polynucleotide and polypeptide may also be used in recombinant DNA
CC constructs, in physical arrays of molecules, as plant breeding markers,
CC or in computer-based storage and analysis systems. The present sequence
CC is a Cotton plant cDNA of the invention. NOTE: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docid=20040181830. However only 6585
CC polynucleotide sequences were available, the remaining 52213
CC polynucleotides and all 58798 protein sequences were not present.
XX
SQ Sequence 1047 BP; 272 A; 217 C; 236 G; 322 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 2,94e-100 Length: 1047
Score: 864.50 Matches: 160
Percent Similarity: 93.78% Conservative: 21
Best Local Similarity: 82.90% Mismatches: 11
Query Match: 86.62% Indels: 1
DB: 13 Gaps: 1
US-10-688-481-11 (1-192) x ADR60523 (1-1047)
Qy 1 MetPhe[leu]Val[Asp]Tyr[Pro]Phe[leu]Val[Ser]Leu[Trp]Gln[Val]Glu 20
Db 221 ATGTTCTTTGGATTGTGTTCTATGAGTGTCTTGTCTCCCTGCTATGACAGAAAGAG 280
Qy 21 Ala[Val]leu[leu]Phe[leu]Gly[Leu]Asp[Asn]Ala[Val]Thr[Thr]Leu[Leu]Met[Leu] 40
Db 281 GCTTAAGATCTTGTCTTCTCGGCTTCGATACCGCGCAAAACACTTGTGCTTCATATGTA 340
Qy 41 Lys[Asp]Glu[Val]Ser[Leu]Gln[His]Gln[Pro]Thr[Glut]Tyr[Pro]Thr[Ser]Glu[Leu]Ser 60
Db 341 AAAGACGAGAGATTGGTTCACCAATCAGCCAACTCAGATCCCAATCGGAGGAAGACTTAAT 400
Qy 61 Ile[Asn]Arg[Val]Lys[Pro]Phe[Val]Ala[Asp]Leu[Val]His[Thr]Leu[Ala]Arg[Val] 80
Db 401 ATTGGAAATCAAGATTCACCAAGCTTTGATTTGGGTGTCTCATGATTTGCTCGTAGTC 460
Qy 81 Trp[Arg]Asp[Tyr]Tyr[Ala]Lys[Val]Asp[Ala]Ile[Val]Tyr[Leu]Val[Asp]Ala[Val]Asp[Arg] 100
Db 461 TGGAAAGATTACATCTATGCTAAGTGATGCTGTGTGATCCGTGATGATGCTCATGATGTA 520
Qy 101 Glu[Arg]Phe[Ala]Glu[Ser]Lys[Val]Glu[Leu]Asp[Ser]Leu[Ser]Asp[Ser]Leu[Ser] 120
Db 521 GAGAGTTTGCAGATGCAAGAAAGAACTCGATCCCTGCTTTCAGACGAGCCCTTGCC 580
Qy 121 Gln[Val]Pro[Val]Leu[Val]Leu[Val]Asn[Val]Ile[Asp]Leu[Pro]Tyr[Ala]Ser[Ser]Glu[Asp] 140
Db 581 AATGTCCCGTTTCTTATCTTACGAAACAGATTCATATACATACGCTGCTCGAGAGAT 640
Qy 141 Glu[Leu]Arg[Pro]Phe[Thr]Leu[Val]Leu[Thr]---Met[Thr]Thr[Val]Gly[Val]Val[Asn]Leu 159
Db 641 GAATTTACGTTACCATCTCCGGCTCACAACTTATCCAGGGCGAGGGAAGTBAACCTA 700
Qy 160 G[AspSer]en[le]a[ArgPro]le[glu]Val[Ph]e[Met]Cys[Ser]le[Val]a[Arg]Leu[Met]Gly 179
Db 701 GCAACATCGAATGTCCTCCCTCAGAGTATTTATGTGCGACATAGATCCGCAAAATGGGA 760
Qy 180 Tyr[glu]glu[glu]Phe[leu]Tyr[Met]Thr[glu]Tyr[leu]Leu 192
Db 761 TATGGGAGCGGCTTAAAGTGAATGTCTCCAAATACATCAAG 799
RESULT 13
AC134445
ID AC134445 standard; cDNA; 876 BP.
XX
XX AC134445;
XX
DT 02-JUN-2005 (first entry)
XX
DE Rice abiotic stress response related polynucleotide SEQ ID NO:13008.
XX
KW ss; abiotic stress tolerance; transgenic plant; plant; cereal;

PR 20-MAY-1999;	99US-0135124P.	PR 02-AUG-1999;	99US-0146386P.
PR 21-MAY-1999;	99US-0135353P.	PR 02-AUG-1999;	99US-0146388P.
PR 24-MAY-1999;	99US-0135629P.	PR 02-AUG-1999;	99US-0146389P.
PR 25-MAY-1999;	99US-0136021P.	PR 03-AUG-1999;	99US-0147038P.
PR 27-MAY-1999;	99US-0136392P.	PR 04-AUG-1999;	99US-0147204P.
PR 28-MAY-1999;	99US-0136782P.	PR 04-AUG-1999;	99US-0147302P.
PR 01-JUN-1999;	99US-0137222P.	PR 05-AUG-1999;	99US-0147192P.
PR 03-JUN-1999;	99US-0137528P.	PR 05-AUG-1999;	99US-0147260P.
PR 04-JUN-1999;	99US-0137502P.	PR 06-AUG-1999;	99US-0147303P.
PR 07-JUN-1999;	99US-0137724P.	PR 06-AUG-1999;	99US-0147416P.
PR 08-JUN-1999;	99US-0138094P.	PR 09-AUG-1999;	99US-0147935P.
PR 10-JUN-1999;	99US-0138540P.	PR 09-AUG-1999;	99US-0147935P.
PR 10-JUN-1999;	99US-0138847P.	PR 10-AUG-1999;	99US-0148171P.
PR 14-JUN-1999;	99US-0139112P.	PR 11-AUG-1999;	99US-0148319P.
PR 16-JUN-1999;	99US-0139452P.	PR 12-AUG-1999;	99US-0148341P.
PR 16-JUN-1999;	99US-0139453P.	PR 13-AUG-1999;	99US-0148655P.
PR 17-JUN-1999;	99US-0139492P.	PR 13-AUG-1999;	99US-0148684P.
PR 18-JUN-1999;	99US-0139454P.	PR 16-AUG-1999;	99US-0149368P.
PR 18-JUN-1999;	99US-0139455P.	PR 17-AUG-1999;	99US-0149175P.
PR 18-JUN-1999;	99US-0139456P.	PR 18-AUG-1999;	99US-0149426P.
PR 18-JUN-1999;	99US-0139457P.	PR 20-AUG-1999;	99US-0149722P.
PR 18-JUN-1999;	99US-0139458P.	PR 20-AUG-1999;	99US-0149723P.
PR 18-JUN-1999;	99US-0139459P.	PR 20-AUG-1999;	99US-0149929P.
PR 18-JUN-1999;	99US-0139460P.	PR 23-AUG-1999;	99US-0149902P.
PR 18-JUN-1999;	99US-0139461P.	PR 23-AUG-1999;	99US-0149930P.
PR 18-JUN-1999;	99US-0139462P.	PR 25-AUG-1999;	99US-0150565P.
PR 18-JUN-1999;	99US-0139463P.	PR 26-AUG-1999;	99US-0150884P.
PR 18-JUN-1999;	99US-0139750P.	PR 27-AUG-1999;	99US-0151065P.
PR 18-JUN-1999;	99US-0139763P.	PR 27-AUG-1999;	99US-0151065P.
PR 21-JUN-1999;	99US-0139817P.	PR 27-AUG-1999;	99US-0151080P.
PR 22-JUN-1999;	99US-0139899P.	PR 30-AUG-1999;	99US-0151303P.
PR 23-JUN-1999;	99US-0140353P.	PR 31-AUG-1999;	99US-0151438P.
PR 23-JUN-1999;	99US-0140354P.	PR 01-SEP-1999;	99US-0151930P.
PR 24-JUN-1999;	99US-0140695P.	PR 07-SEP-1999;	99US-0152363P.
PR 28-JUN-1999;	99US-0140823P.	PR 10-SEP-1999;	99US-0153070P.
PR 29-JUN-1999;	99US-0140991P.	PR 13-SEP-1999;	99US-0153758P.
PR 30-JUN-1999;	99US-0141287P.	PR 15-SEP-1999;	99US-0154018P.
PR 01-JUL-1999;	99US-0141842P.	PR 16-SEP-1999;	99US-0154039P.
PR 01-JUL-1999;	99US-0142154P.	PR 20-SEP-1999;	99US-0154779P.
PR 02-JUL-1999;	99US-0142055P.	PR 22-SEP-1999;	99US-0155139P.
PR 06-JUL-1999;	99US-0142390P.	PR 23-SEP-1999;	99US-0155486P.
PR 08-JUL-1999;	99US-0142803P.	PR 24-SEP-1999;	99US-0155659P.
PR 09-JUL-1999;	99US-0142920P.	PR 28-SEP-1999;	99US-0156458P.
PR 12-JUL-1999;	99US-0142977P.	PR 29-SEP-1999;	99US-0156596P.
PR 13-JUL-1999;	99US-0143542P.	PR 04-OCT-1999;	99US-0157117P.
PR 14-JUL-1999;	99US-0143624P.	PR 05-OCT-1999;	99US-0157753P.
PR 15-JUL-1999;	99US-0144005P.	PR 06-OCT-1999;	99US-0157865P.
PR 16-JUL-1999;	99US-0144085P.	PR 07-OCT-1999;	99US-0158029P.
PR 16-JUL-1999;	99US-0144086P.	PR 08-OCT-1999;	99US-0158232P.
PR 19-JUL-1999;	99US-0144325P.	PR 12-OCT-1999;	99US-0158369P.
PR 19-JUL-1999;	99US-0144331P.	PR 13-OCT-1999;	99US-0159293P.
PR 19-JUL-1999;	99US-0144332P.	PR 13-OCT-1999;	99US-0159294P.
PR 19-JUL-1999;	99US-0144333P.	PR 13-OCT-1999;	99US-0159295P.
PR 19-JUL-1999;	99US-0144334P.	PR 14-OCT-1999;	99US-0159329P.
PR 19-JUL-1999;	99US-0144335P.	PR 14-OCT-1999;	99US-0159330P.
PR 20-JUL-1999;	99US-0144352P.	PR 14-OCT-1999;	99US-0159331P.
PR 20-JUL-1999;	99US-0144632P.	PR 14-OCT-1999;	99US-0159637P.
PR 20-JUL-1999;	99US-0144884P.	PR 14-OCT-1999;	99US-0159638P.
PR 21-JUL-1999;	99US-0144814P.	PR 18-OCT-1999;	99US-0159584P.
PR 21-JUL-1999;	99US-0144865P.	PR 21-OCT-1999;	99US-0160741P.
PR 21-JUL-1999;	99US-0145088P.	PR 21-OCT-1999;	99US-0160767P.
PR 22-JUL-1999;	99US-0145087P.	PR 21-OCT-1999;	99US-0160770P.
PR 22-JUL-1999;	99US-0145089P.	PR 21-OCT-1999;	99US-0160814P.
PR 22-JUL-1999;	99US-0145192P.	PR 21-OCT-1999;	99US-0160815P.
PR 23-JUL-1999;	99US-0145145P.	PR 22-OCT-1999;	99US-0160980P.
PR 23-JUL-1999;	99US-0145224P.	PR 22-OCT-1999;	99US-0160981P.
PR 26-JUL-1999;	99US-0145276P.	PR 25-OCT-1999;	99US-0161404P.
PR 27-JUL-1999;	99US-0145913P.	PR 25-OCT-1999;	99US-0161405P.
PR 27-JUL-1999;	99US-0145918P.	PR 26-OCT-1999;	99US-0161359P.
PR 28-JUL-1999;	99US-0145951P.	PR 26-OCT-1999;	99US-0161360P.

PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161992P.
 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:

Pred. No.:	4,17e-100	Length:	885
Score:	862.50	Matches:	160
Percent Similarity:	93.78%	Conservative:	21
Best Local Similarity:	82.90%	Mismatches:	11
Query Match:	86.42%	Indels:	1
DB:	3	Gaps:	1

US-10-688-481-11 (1-192) x AAC42538 (1-885)

QY 1 MetPheLeuValAspTyrPheTyrGlyPheLeuAlaSerIleGlyLeuTyrGlnVal 20
 Db 94 ATGTTTCATGATCGATGTTCTTATGGCGTTCTCGCTTCGTATAGGTTATGCGAAGAG 153
 QY 21 AlAlaGlyIleuPheLeuGlyLeuAspAsnAlaGlyIleThrThrLeuLeuHISmetLeu 40
 Db 154 GCTAAGATCTTGTCTTGGGACCTCGATTAATGCTGTAACCACTCTGCTTCACTGTTG 213
 QY 41 LysAspGluIleuPheLeuGlyGlnHISGlnProThrGlnTyrProThrSerGluLeuSer 60
 Db 214 AAGAGACAGAGATGTTGTTACGATCAGCATCAGCATCAGCATCAGCATCAGCATCAGC 273
 QY 61 ILAsnArgValIleuPheLeuGlyAlaPheAspLeuGlyIleThrIleAlaArgArgVal 80
 Db 274 ATTGGGAAATCAAGTTTAAGGCTTTGATTTGGGTGTCAACGATTTGCTCGAGGCTC 333
 QY 81 TrpArgAspTyrTyrAlaValValAspAlaIleValTyrLeuValAspAlaValAspArg 100
 Db 334 TGGAGAGATTACTATGCTTAAGTGGACGCTGTGCTTACCTAGTGTGCTTACGACAAA 393
 QY 101 GluArgPheAlaGluSerIleuValGluLeuAspSerLeuSerAspAspSerLeuSer 120
 Db 394 GAGGATTTCCAGATCAAAAGAAAGAACTGATGACCTTCTCTCAGACGAATCCCTTACC 453
 QY 121 GlnValProValIleuValIleuGlyAsnIleuAspIleProTyrAlaSerSerGluAsp 140
 Db 454 AGGTTTCATTCTCCTCATTTAGGAAACAGATGACATACGATGCTGATCAGAGAC 513
 QY 141 GluLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyGlyThrValAsnLeu 159
 Db 514 GAGCTCCGTTACCATCTCGGCTCTCCACACTTCACTACAGAAAGGCTAAAGTGAATCTA 573
 QY 160 GlysAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgIleMetGly 179
 Db 574 ACGGATTTCGAACGTTAGGCCATTTGAGGTTTCAATGTGACGATTTGACGAAATAGGCT 633
 QY 180 TyrGlyGluGlyPheLeuTyrMetThrGlnTyrIleLeu 192
 Db 634 TACGAGAAAGTTTCAATGAGTTTCCATACATCAATCAAG 672

RESULT 15
 ABK71577
 ID ABK71577 standard; cDNA; 928 BP.
 AC ABK71577;
 XX 30-JUL-2002 (first entry)
 XX Human dlthp polynucleotide #43.
 XX Human; dlthp; diagnostic and therapeutic polynucleotide; gene; ss; bone; cell proliferative disorder; cancer; tumour; autoimmune disorder; brain; inflammatory disorder; viral infection; bacterial infection; seizure; fungal infection; parasitic infections; developmental disorder; breast; endocrine disorder; metabolic disorders; neurological disorder; cervix; gastrointestinal disorder; transport disorder; gene therapy; kidney; adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;

KM skin; testis; thymus.
 XX
 OS Homo sapiens.
 XX
 PN WO200220754-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 29-AUG-2001; 2001MO-US027127.
 XX
 XX 05-SEP-2000; 2000US-0229747P.
 XX 05-SEP-2000; 2000US-0229748P.
 XX 05-SEP-2000; 2000US-0229749P.
 XX 05-SEP-2000; 2000US-0229750P.
 XX 05-SEP-2000; 2000US-0229751P.
 XX 05-SEP-2000; 2000US-0230583P.
 XX 06-SEP-2000; 2000US-0230505P.
 XX 06-SEP-2000; 2000US-0230514P.
 XX 06-SEP-2000; 2000US-0230515P.
 XX 06-SEP-2000; 2000US-0230517P.
 XX 06-SEP-2000; 2000US-0230518P.
 XX 06-SEP-2000; 2000US-0230519P.
 XX 06-SEP-2000; 2000US-0230597P.
 XX 06-SEP-2000; 2000US-0230597P.
 XX 06-SEP-2000; 2000US-0230597P.
 XX 06-SEP-2000; 2000US-0230599P.
 XX 06-SEP-2000; 2000US-0230610P.
 XX 06-SEP-2000; 2000US-0230865P.
 XX 06-SEP-2000; 2000US-0230988P.
 XX 07-SEP-2000; 2000US-0230951P.
 XX 07-SEP-2000; 2000US-0231163P.
 XX 07-SEP-2000; 2000US-0231167P.
 XX
 PA (INCYTE) INCYTE GENOMICS INC.
 XX
 PI Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JR;
 PI Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PB, Dahl CR;
 PI Momiyama MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM;
 PI Gerstein EH, Peralta CH, David MH, Panzer SR, Flores V, Delfo A;
 PI Marwaha R, Chen AJ, Chang SC, Au AP, Imman RR;
 XX
 DR WPI; 2002-383054/41.
 DR P-PDB; ABG59985.
 XX
 PT An isolated polynucleotide useful in diagnostics and therapeutics.
 XX
 PS Claim 1; Page 427; 686pp; English.
 XX
 CC The invention relates to human diagnostic and therapeutic (dlthp)
 CC polynucleotides and their associated polypeptides (dlthp polypeptides).
 CC The sequences of the invention are used in the treatment and diagnosis of
 CC cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
 CC (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast,
 CC cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or
 CC thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,
 CC psoriasis, osteoporosis), viral infections, bacterial infections, fungal
 CC infections, parasitic infections, developmental disorders (e.g. anaemia,
 CC epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),
 CC endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders
 CC (e.g. obesity, diabetes), neurological disorders (e.g. stroke,
 CC amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal
 CC disorders (e.g. ulcerative colitis, lymphoma) and transport disorders
 CC (e.g. myotonic dystrophy, catatonis, peripheral neuropathy). Sequences
 CC ABK71535-ABK71809 represent human dlthp polynucleotides of the invention
 XX
 SQ Sequence 928 BP; 206 A; 251 C; 262 G; 209 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 4.46e-100 Length: 928
 Score: 862.50 Matches: 160
 Percent Similarity: 93.78% Conservative: 21
 Best Local Similarity: 82.90% Mismatches: 11
 Query Match: 86.42% Indels: 1

DB:	6	Gaps:	1
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US-10-688-481-11 (1-192) x ABK71577 (1-928)

QY MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTppGlnLysGlu 20
Db ATGTTCTCTGGGACTGGATTCTACGGGGAGTGGTGGCTTCTCCCTGGACTGTGGCAAGAGAG 222
QY AAlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHisMetLeu 40
Db GGCAAGATCTCTTCTCTTGGCCTCGACCAAGCGGGCAAGCCAGCGTGGCTCCAGATGCTC 282
QY LysAspGlyLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGlyGluLeuSer 60
Db AAGGACGAGCGGTGGTGGCAGACCCAGCCGACACCCGACCGTGGAGGAGCTCAGC 342
QY IleAsnArgValLysPheLysAlaPheAspLeuGlyGlnHisThrIleAlaArgVal 80
Db ATCGGCAAGATCAAGTTCAAAGGGGTTCGACTGGGGGCCACCAAGATGGCGCGCGGTG 402
QY TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db TCGAAGGATTACTACCCAAAGGTGATGCTGTAGTATCCTGGTATGATGATGATGATG 462
QY GlnArgPheAlaGluSerLysGlyLeuAspSerLeuLeuSerLysAspAspSerLeuSer 120
Db GAGCATTTGTGTAATCAAAAGAGAGAGCTCGATGCTCTCTGTGTATGATGATCTTTGGCC 522
QY GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrLysSerGluAsp 140
Db AATGTTCATTTCTCTCATCTTGGCAACAGATTGATATCCCATATGCTGCTTGAAGAG 582
QY GlnLeuArgPheThrLeuGlyLeuThr---MetThrThrGlyLysGlyThrValAsnLeu 159
Db GAGCTACGGTATCACCTAGGCTTACCACTTACCAACCGGAAAGGCCAAGCTCAACTT 642
QY GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValAlaArgLysMetGly 179
Db GCGGACTCCAAATGTCGCTCCACTTGAAGTCTTCATGTGCGAGTGTGTTGCCAAGATGGGC 702
QY TyrGlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
Db TACGGTGATGTTCAAGTGGGTCTCCCAAGTATCATCAAG 741

Search completed: December 9, 2005, 01:50:23
Job time : 473 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 01:39:43 ; Search time 3745 Seconds
(without alignments)
2398.697 Million cell updates/sec

Title: US-10-688-481-11

Perfect score: 998
Sequence: 1 MFLVDFYGYGLASIGLWKE.....SIVRKKGYGEGFKMTQYIK 192

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgrt_1/USPTO.spool_p/US10688481/runat_05122005_094812_15857/app.query.fasta_1.391
-DB=EST -QPM=faaap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-DEVS-bits -START=1 -END=1 -MATRIX=blom62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFM=ptco -NORM=exc -HEAPSIZE=500 -MINLEN=50 -MAXLEN=200000000
-USR=US10688481.OCGN_1_1-8010.0runat_05122005_094812_15857 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: *
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_est8:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	DB ID	Description
No.					
C 1	974	97.6	607	3	BJ952512 BJ952512
C 2	974	97.6	650	3	BJ599136 BJ599136
C 3	974	97.6	734	3	BJ598350 BJ598350
C 4	974	97.6	740	3	BJ609449 BJ609449
5	880.5	88.2	638	5	BJ0037417 946138P10
6	880.5	88.2	669	5	BJ0098049 946123E11
7	880.5	88.2	720	7	COS26683 3530_1.17

C	8	880.5	88.2	724	5	BQ779008	BQ779008	946116C06
	9	880.5	88.2	749	3	BJ572166	BJ572166	BJ572166
	10	880.5	88.2	830	3	DR829325	DR829325	2M_BPB007
	11	880.5	88.2	877	8	DR824574	DR824574	2M_BPB006
	12	880.5	88.2	903	7	CO443833	CO443833	MZCCL1006
	13	880.5	88.2	1098	4	AY106333	AY106333	2M_mays
	14	880.5	88.2	861	7	CN206979	CN206979	TOY739 Ga
	15	877.5	87.2	807	8	DN152566	DN152566	5207_C08
	16	870.5	87.2	622	7	CV300967	CV300967	ESTR88310
	17	868.5	87.0	724	7	CV472407	CV472407	45743_1 C
	18	868.5	87.0	793	5	BM688373	BM688373	BM688373
	19	868.5	87.0	800	2	BG887226	BG887226	EST513077
	20	868.5	87.0	882	2	BF460011	BF460011	071G06 Ma
	21	868.5	87.0	885	8	DN168126	DN168126	LH_Ea02M
	22	867.5	86.9	755	8	CM724867	CM724867	EST5007 Z
	23	866.5	86.8	650	5	CA015435	CA015435	HT14E23T
	24	866.5	86.8	673	3	BU226471	BU226471	BU226471
	25	866.5	86.8	682	5	BQ839446	BQ839446	WHB416-B
	26	866.5	86.8	692	5	BQ805647	BQ805647	WHE3569_D
	27	866.5	86.8	700	1	AL505462	AL505462	AL505462
	28	866.5	86.8	700	5	BQ471183	BQ471183	HVO1H06T
	29	866.5	86.8	708	6	CD869290	CD869290	AZ02_111B
	30	866.5	86.8	724	6	CA174544	CA174544	SCUFT101
	31	866.5	86.8	783	7	CK123056	CK123056	BSB182410
	32	866.5	86.8	1159	8	DR740572	DR740572	FGAS00051
	33	865.5	86.7	629	2	BG350081	BG350081	083D01 Ma
	34	865.5	86.7	646	2	BE494747	BE494747	WHE1272 G
	35	865.5	86.7	675	5	BQ407022	BQ407022	GA_Ea010
	36	865.5	86.7	695	6	CD880780	CD880780	F1_075N23
	37	865.5	86.7	702	3	BQ112215	BQ112215	EST579791
	38	865.5	86.7	728	3	B1434155	B1434155	EST536916
	39	865.5	86.7	735	8	DR035154	DR035154	18581.2 S
	40	865.5	86.7	758	6	CD905083	CD905083	GA68_100H
	41	865.5	86.7	834	7	CV302973	CV302973	75006.1 S
	42	865.5	86.7	859	1	AJ822454	AJ822454	AJ822454
	43	864.5	86.6	589	6	CA825610	CA825610	R62D03 tw
	44	864.5	86.6	636	5	BU827781	BU827781	K008P84P
	45	864.5	86.6	642	8	DN180683	DN180683	HO26C22S

ALIGNMENTS

RESULT 1
BJ952512/c 607 bp mRNA linear EST 14-JUN-2005
LOCUS BJ952512 phnf full-length cDNA library Physcomitrella patens subsp.
DEFINITION BJ952512 patens cDNA clone phnf1p22.3', mRNA sequence.
ACCESSION BJ952512
VERSION BJ952512.1 GI:67692279
KEYWORDS EST.
SOURCE Physcomitrella patens subsp. patens
ORGANISM Physcomitrella patens subsp. patens
REFERENCE
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
1 (bases 1 to 607)
Fujita,T., Nishiyama,T., Shin-i,T., Koharz,Y. and Hasebe,M.
Physcomitrella patens subsp. patens
division of protoplasts
Unpublished (2005)
Contact: Tadao Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@gene.nig.ac.jp

Protonemata were inoculated on BCDANG medium for every ca. 5 days. Protoplasts were isolated from the protonemata, further incubated at 25C under continuous light for 2-3 days. The regenerated cells, which were rich in cells at a stage during the first asymmetric cell division, were collected. Total RNA was extracted for constructing a full-length cDNA library. The database of the EST clones is available at the PHYSCobase (<http://moss.nibb.ac.jp>).


```

FEATURES
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        Location/Qualifiers
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                /organism="Physcomitrella patens subsp. patens"
                /mol_type="mRNA"
                /sub_species="patens"
                /db_xref="taxon:145481"
                /clone="pPh16p22"
                /tissue_type="regenerated protoplasts (chloronemata)"
                /dev_stage="at the first asymmetric cell division of
                protoplasts"
                /clone_lib="pPhf full-length cDNA library"
                /note="Protonemata were inoculated on BCD496 medium for
                every ca. 5 days. Protoplasts were isolated from the
                protonemata, further incubated at 25C under continuous
                light for 2-3 days. The regenerated cells, which were rich
                in cells at a stage during the first asymmetric cell
                division, were collected. Total RNA was extracted for
                constructing a full-length cDNA library."

ORIGIN
Alignment Scores:
Pred. No.:      3,286-115      Length:      607
Score:          974.00      Matches:      186
Percent Similarity: 98.96%      Conservative: 4
Best Local Similarity: 96.88%      Mismatches: 2
Query Match:     97.60%      Indels:      0
DB:              3      Gaps:      0

US-10-688-481-11 (1-192) x BU592512 (1-607)

Qy      1  MetPheLeuValAspTTPheTYrGlyPheLeuAlaSerIleGlyLeuTrpGlnLysGlu 20
Db      580  ATGTTTATCGTAGATGTTGTTTATGCGCTTCTTCGCGAGCATAGGTTGTGCGAAGAGAG 521
Qy      21  AlAlaValIleLeuPheLeuGlyLeuAspAspAlaGlyLysThrThrLeuLeuHISMetLeu 40
Db      520  GCCAAATCTGTCTCGGTCTTGACATCCGCGAAGAGACACTTCTGCAACATGCTC 461
Qy      41  LysAspGluLysLeuGlyGlnHISGlnProThrGlnTYrProThrSerGluGluLeuSer 60
Db      460  AAGCATGAGAACTCGGGCAACATCAACCAACGAGTATCCAACTCTGAAGATTGAGC 401
Qy      61  IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHISThrIleAlaArgArgVal 80
Db      400  ATCAATAGGCTGAGATTCAAGCAATTCGATCTAGGTGCTCACGATGCTCGACGTGTG 341
Qy      81  TrpArgAspTYrTYrAlaLysValAspAlaIleValTYrLeuValAspAlaValAspArg 100
Db      340  TGGAGGGACTACTATGCTTAAGGTGATGCTATCGTTTACCTTGTCGACGCGATTGACAG 281
Qy      101  GluArgPheAlaGluSerLysLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
Db      280  GAGAGGTTTCTCGAATCAAAAGAAAGAACTCCATCTTGCTCTGAGAGACTCCGCTCC 221
Qy      121  GlnValProValLeuValLeuGlyAsnLysIleAspIleProTYrAlaSerSerGluAsp 140
Db      220  CAATGCTGCTGCTGCTCTTGGCAACAAAGATTGACATCCCTTACGCTGCCGAGAGAT 161
Qy      141  GluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyLysGlyThValAsnLeuGly 160
Db      160  GAATTCGCGTACACCTCGGCTGACCAATGACCACTGGCAAGAAAGCGTAAACCTGAAG 101
Qy      161  AspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGlyTYr 180
Db      100  GATAGCAACATCCGGCCCATTTGAGGTTTTCATGTGCATATAGTCGTAAGATGGGTTAC 41
Qy      181  GlyGluGlyPheLysTrpMetThrGlnTYrIleLys 192
Db      40  GCGCAAGGCTCAAGTGTGATGACGAGATATTTAA 5

RESULT 2
BU59136/c      BU599136      650 bp      mRNA      linear      EST 22-OCT-2003
LOCUS

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DEFINITION
BU599136 normalized full length cDNA library, chloronemata,
caulonemata and rhizoid-like protonemata Physcomitrella patens
subsp. patens cDNA clone pPhn25113 3', mRNA sequence.

ACCESSION
BU599136
VERSION
BU599136.1 GI:37841128
KEYWORDS
EST.
SOURCE
Physcomitrella patens subsp. patens
ORGANISM
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
1 (bases 1 to 650)
Nishiyama,T., Fujita,T., Shin-I,T., Seki,M., Nishide,H.,
Uchiyama,T., Kamiya,A., Carninci,P., Hayashizaki,Y., Shinozaki,K.,
Kohara,Y. and Hasebe,M.
Comparative genomics of Physcomitrella patens gametophytic
transcriptome and Arabidopsis thaliana: implication for land plant
evolution
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
JOURNAL
PUBMED
12808149
COMMENT
Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp
A backbone of the vector is basically from pBluescript II (KS),
that was in vivo excised from a 1-F1C phage vector (Carninci et al.,
2001). 5' end of the cDNA that was digested with XhoI was ligated
to SalI site of the vector and the 3' end including polyA tail was
ligated to BamHI site of the
vector(5'- GAGAGAGAGAGATCCACCTG9AGAGTTTTTTTTTTTTTTVN-3' was
used as a 1st 3' primer, and
5'-GGTCTCGAGTCATCGTGTCCAGACGAGTACTCGAAGACGANNNN-3' as 2nd
5'-hairpin primer giving the following 5' boarder sequence.
AGGCCAATCGCCGACGATTCGATTCGTGAGAACGG). cDNA insert could be
amplified with conventional T7 and T3 primers. This full-length
cDNA library was generated according to the method described in
Nishiyama et al. (2003).
Protonemata were blended by the POLYTRON, and then cultivated on
the BCD496 medium for 13-14 days under the continuous light.
These clones are available from RIKEN Bio Resource Center
(http://www.brc.riken.go.jp/lab/epd/Eng/index.html). The database
of Physcomitrella EST clones is available at the PHYSCODbase
(http://mose.nibb.ac.jp).

FEATURES
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        Location/Qualifiers
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                /mol_type="mRNA"
                /sub_species="patens"
                /db_xref="taxon:145481"
                /clone="pPhn25113"
                /tissue_type="mixture of chloronemata, caulonemata and
                rhizoid-like protonemata"
                /clone_lib="normalized full length cDNA library,
                chloronemata, caulonemata and rhizoid-like protonemata"

ORIGIN
Alignment Scores:
Pred. No.:      3,616-115      Length:      650
Score:          974.00      Matches:      186
Percent Similarity: 98.96%      Conservative: 4
Best Local Similarity: 96.88%      Mismatches: 2
Query Match:     97.60%      Indels:      0
DB:              3      Gaps:      0

US-10-688-481-11 (1-192) x BU599136 (1-650)

Qy      1  MetPheLeuValAspTTPheTYrGlyPheLeuAlaSerIleGlyLeuTrpGlnLysGlu 20
Db      603  ATGTTTATCGTAGATGTTTATGCGCTTCTTCGCGAGCATAGGTTGTGCGAAGAGAG 544
Qy      21  AlAlaValIleLeuPheLeuGlyLeuAspAspAlaGlyLysThrThrLeuLeuHISMetLeu 40

```


Db	543	GCCAAATCTTGTCTCTGGCTTGTACAAATCGCGGAAGACACCTTCTGCACATGCTC	484
Qy	41	LYSAPGILVLSLEUGLYGNIHISGINDPROTHRGINTYRPROTHSERGIUGILEUSER	60
Db	483	AAGATGAGAAATCGGGCAACATCAACCAACGAGTATCCAAATCGAAGATTGAGC	424
Qy	61	ILEASNATGVALVSRPHELYGALAPHEASPLEUGLYGIIYHISTHIIIEALATRGATGYAL	80
Db	423	ATCATATAGGGGAAAGTTCCAAAGCATTCATCTAGGTGTGCACACATTTGCTCGAGGTGG	364
Qy	81	TPRATGAPPTYYRYRALALYSVALASPAIAIIEVALIYRLEUVALASPAIAVALASPARG	100
Db	363	TGGAGGACCTATGCTTAGGTGGATGCTATCGTTACCTTGTGACCGCAGTTGACAAAG	304
Qy	101	GLIURGPHEALAGIUSERLYSGLILEUASPSEULEUSERASPAASPERLEUSER	120
Db	303	GAGAGGTTCTCCGATCAAGAAAGAACCTCGACTCTTCGATGACTCGCTCTCC	244
Qy	121	GLINVALPROVALLEUVALLEUGLYASNLYSIIIEAPPIIEPROTYRALASERERGLUAP	140
Db	243	CAAGTGGCTGTGCTGGTCTCTGGCAACAAGATTGACATCCCTTACGCTGCCCTCCAGAGT	184
Qy	141	GLIUEUATRGPHETNLEUGLYLEUTHRMETTHTRHGIYLYSGIYTHRVALASMLEUGLY	160
Db	183	GAATTGCGGTACACACTCGGCTGACCTGACCACTGGCAANAGAACGGTGAACCTGGAAG	124
Qy	161	ASPSEKASNIIEATRGPROILEGIVALEPHEMETCYSEKIIIEVALIARGLYSMETGLIYTR	180
Db	123	GATAGCAACATCCGGCCATTGAAGGTTTTCATGTGCAGATATAGTCGTAAAGATGGATTAC	64
Qy	181	GLIYGLUGLYRHELYSTRPMETTHCINLYRIILELYS	192
Db	63	GGCGAAGGGTTCAGGTGATGACGACGATATATTAA	28

RESULT 4
Bj609449/c

LOCUS 740 bp mRNA linear EST 22-OCT-2003

DEFINITION Bj609449 normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata Physcomitrella patens subsp. patens cDNA clone pphn47g10 3', mRNA sequence.

ACCESSION Bj609449

VERSION Bj609449

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

12808149

Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp

A backbone of the vector is basically from pBluescript II (KS), that was in vivo excised from a 1-F1C phage vector (Carninci, et al., 2001). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector (5'-gagagagagagatccacacctgagagatgtttttttttttttt-3' was used as a 1st 3' primer, and

5'-ggtttctgcagtcgctcgttccagacagagatgacgcgaaccgannnn-3' as 2nd 5', hairpin primer, giving the following 5 boarder sequence,
AGGCCAATCGCGCGACGCTCGAATTCGTCAAGACCG). cDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated according to the method described in Nishiyama et al. (2003).

Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (<http://www.brc.riken.go.jp/lab/epd/eng/index.html>). The database of Physcomitrella EST clones is available at the PHYSCOBASE (<http://mes.nibb.ac.jp>).

Location/Qualifiers

1. 740

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/db_xref="taxon:145481"
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/tissue_type="mixture of chloronemata, caulonemata and rhizoid-like protonemata"
/clone_lib="normalized full length cDNA library",
chloronemata, caulonemata and rhizoid-like protonemata"

ALIGNMENT SCORES

pred. No.: 4,34e-115 Length: 740
Score: 974.00 Matches: 186
Percent Similarity: 98.96% Conservative: 4
Best Local Similarity: 96.88% Mismatches: 2
Query Match: 97.60% Indels: 0
DB: 3 Gaps: 0

US-10-688-481-11 (1-192) x Bj609449 (1-740)

ORIGIN

1 MetPrelEValAAsPTPhPhyTelyPheLenaIAserIlleglyVleuTrpGlnlyGlu 20

Db	Accession	Source	Organism	Reference Authors	Journal Comment	Features
Db	605	ATGTTATCGAGATTGGTTTATGAGCTTTCGCGAGCATAGGTTGTGGCGAAGAG	546			
Qy	21	AlaAlysIleuPheLeuGlyLeuAspAsnAlaGlyIySerThrIleuLeuHisMetLeu	40			
Db	545	GCCAAATCTTGTCCTGGGCTTGAACAATGCCGGGAAGCGACATCTTGCAATGCTC	486			
Qy	41	LysAspGluIySLeuGIyGlnHisGlnProThrGlnTyrProThrsSerGluGluSer	60			
Db	485	AAGATGAGAACTCGGGGCAACATCAACGACGAGATCCACATCTGAAGAATTGAC	426			
Qy	61	IleAsnArgValIySPhelysAlaPheAspLeuGIyGlnHisThrIleAlaArgVal	80			
Db	425	ATCATATAGGGGAGAGTTCAAAGCATTCGATCTAGTGATGTCACAGATTGCTCGAGTGC	366			
Qy	81	ThrPArgSerPyrTyrAlaIySValAspAlaIleValIyIleuValAspAlaValAspArg	100			
Db	365	TGGAGGCACTACTTGTGCTAAGTGGAGTCACTCTTACCTTGCGACGAGTTGACAG	306			
Qy	101	GluArgPheAlaGluSerIySValGluLeuAspSerLeuSerAspAspSerLeuSer	120			
Db	305	GAGAGGTTTCTGTAATCAAGAAAGAACTGCACTCTTCTCTCGATGACTGCTTCC	246			
Qy	121	GlnValProValIleuValIleuGIyAsnIySAlaAspIleProTyrAlaSerSerGluAsp	140			
Db	245	CAATGCTGTCGTGCTGCTTGGCAACAGATTACATCCCTTAACGCTGCCGGAAGAT	186			
Qy	141	GluLeuArgPheThrIleuGIyLeuThrMetThrThrGlyIySgIyThrValAsnLeuGIy	160			
Db	185	GAATTGGCTGCACACACTCGGCTGACCATGCACTGGCAAGAGAGCGTGAACCTGAG	126			
Qy	161	AspSerAsnIleAspProIleGluValPheMetCysSerIleValArgIyMetGlyTyr	180			
Db	125	GATGCAACATCCGGCCCATGAGGTTTCAATGTCAGTATAGTCCGTAGAGATGGATTAC	66			
Qy	181	GlyGluGIyPheIySTrpMetThrGlnTyrIleIyS	192			
Db	65	GGCGAAGGTTCAAGTGGATGACCCAGATATTATAA	30			
RESULT 5	BU037417	638 bp	mRNA	linear	EST 23-AUG-2002	
LOCUS	946138F10.y1.946	- tassels	primordium	prepared by	Schmidt lab	Zea
DEFINITION	mays cDNA, mRNA sequence.					
ACCESSION	BU037417					
VERSION	BU037417.1	GI:22472937				
KEYWORDS	EST.					
SOURCE	Zea mays					
ORGANISM	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.					
REFERENCE	1 (bases 1 to 638)					
AUTHORS	Walbot, V.					
TITLE	Mays ESTs from various cDNA libraries sequenced at Stanford University					
JOURNAL	Unpublished (1999)					
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 946138 row: F column: 10.					
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	/describes="just after the transition from vegetative to inflorescence development"					

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 DB 481 GCCGACTCCAAAGCCGCGCCCTGAGATCTTCATGTGCAAGTGTGGCCAAAGATGGC 540
 QY 180 TyrGlyGluGlyPheLysTrpMetThrGlnTyrIleLeu 192
 DB 541 TATGGCGAAGGCTTCAATGATGTCTCAGTACATCAAG 579

RESULT 7
 LOCUS COS26683 720 bp mRNA linear EST 15-JUL-2004
 DEFINITION 3530_1177_1.E04.y.1.3530 - Full length cDNA library created by
 INVITROGEN from multiple tissues Zea mays cDNA, mRNA sequence.
 ACCESSION COS26683
 VERSION COS26683.1 GI:50331557
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 720)
 Maiboc V.
 Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 Unpublished (1999)
 CONTACT: Maiboc V.
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walboc@stanford.edu
 Plate: 3530.1.177.1 row: E column: 04.
 Location/Qualifiers
 1..720
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /tissue_type="multiple"
 /dev_stage="varies by tissue"
 /lab_host="DH10B"
 /clone_id="3530 - Full length cDNA library created by
 INVITROGEN from multiple tissues"
 /note="Organ: silks, husks, ears, pollen, shoot tips,
 leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT
 6.1; Site_1: EcorV; Site_2: NotI; Maize Gene Discovery
 Project contracted with INVITROGEN to produce a
 normalized, full length library in a pSPORT vector. This
 is a Gateway compatible vector, permitting clone movement
 to new vector backbones for expression in diverse host
 cells using recombination rather than restriction enzymes.
 Details of the vector and sequencing primers are available
 at ZMDB in the EST library description tables. poly(A)+
 mRNA was prepared by INVITROGEN, and equimolar amounts of
 RNA from each of the 12 tissue samples were mixed together
 for selection of mRNA with a 5' cap. After synthesis of
 cDNA, a normalization step was conducted against the
 mixture of RNA sources. This step effected a 20X to 80X
 reduction in common transcript types. Tissues prepared: 1.
 just emerging silks; 2. inner husks from ears of sample
 #1; 3. 20 day aleurone; 4. immature tassels, stages from
 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm
 vegetative shoot tips from 15 day old seedlings; all
 leaves with an expanded or partially expanded sheath
 were removed; 8. mature leaf tissue; 9. 0.5 cm long root
 tips from 15 day old seedlings; 10. 10 day whole seed; 11.
 12 day endosperm and embryo; 12. 17 day endosperm and
 embryo. All of the sequenced clones in project 3530 will
 be archived at the University of Arizona along with the
 UniGene clones from the Maize Gene Discovery EST

sequencing projects. Clones can be ordered through the
 ZMDB web site or directly from the University of Arizona
 (<http://www.genome.arizona.edu/orders/>). High density
 filters containing over 18,000 clones can also be ordered
 from the University of Arizona."

ORIGIN
 Alignment Scores:
 Pred. No.: 5,36e-103 Length: 720
 Score: 880.50 Matches: 163
 Percent Similarity: 94.30% Conservative: 19
 Best Local Similarity: 84.46% Mismatches: 10
 Query Match: 88.23% Indels: 1
 DB: 7 Gaps: 1

US-10-688-481-11 (1-192) x COS26683 (1-720)

QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnGlu 20
 DB 100 ATPTCTCGTGGAGCTGTCTATGAGGCTGCTGACATCGCTTGCGCAAGAG 159
 QY 21 AlaLysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHISMetLeu 40
 DB 160 GCTAAGATCTCTTCTTGCCCTCGACACGCCGGCAAGCAACCCCTCCACATGCTG 219
 QY 41 LysAspGlnLysLeuGlyGlnHisGlnProThrGlnTyrProThrsersGlnLeuSer 60
 DB 220 AAGGACGAGCGCTCGTACAGCACACGCCACAGTACCCACGTCAGAAAGTTGAGC 279
 QY 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgArgVal 80
 DB 280 ATCGCGAGATCAAGATTCAAGGCGTTGCTGAGTGGGGCCACCAAGTCCGCCGCGTTC 339
 QY 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
 DB 340 TCGAAGACACTACACCGCAAGCTTGATGCTGTGTGATCTGTGATGATGCTGTGACAG 399
 QY 101 GluArgPheAlaGluSerLysLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
 DB 400 GAACGTTTCCGAGTCGAAGAAAGAGAGCTTGAGCGCTTCTTCAGATGACTCCCTTGCA 459
 QY 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
 DB 460 AAGCTTCCTTCTCTCACTGCGCAACAGATGACATCCCATRACGCGGCTTCAGAGAG 519
 QY 141 GluLeuArgPheThrLeuGlyLeuThr---MetThrThrGlyLysGlyThrValAsnLeu 159
 DB 520 GAGGTGAGTACTACTCGGCTCGACCACTTCACAAACCGGAAGCAACGTGAATTG 579
 QY 160 GlyaSpSerAniLeaPProIIeGluValPheMeCySerIleValAlaGlyMeGly 179
 DB 580 GCCGACTCCAAAGCCGCGCCCTGAGATCTTCATGTGCAAGTGTGGCCAAAGATGGC 639
 QY 180 TyrGlyGluGlyPheLysTrpMetThrGlnTyrIleLeu 192
 DB 640 TATGGCGAAGGCTTCAATGATGTCTCAGTACATCAAG 678

RESULT 8
 LOCUS B0779008 724 bp mRNA linear EST 26-JUL-2002
 DEFINITION 946116C06.y1.946 - tassels primordium prepared by Schmidt lab Zea
 mays cDNA, mRNA sequence.
 ACCESSION B0779008
 VERSION B0779008.1 GI:21987480
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 724)
 Maiboc V.
 Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL
COMMENT

University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946116 row: C column: 06.

FEATURES

source

1. 724
/organism="Zea mays"
/mol_type="mRNA"
/cuiivar="OH43"
/db_xref="taxon:4577"
/tissue_type="tassel"
/dev_stage="just after the transition from vegetative to inflorescence development"
/lab_host="XLOLR"
/clone_lib="946 - tassel primordial prepared by Schmidt lab"
/note="Organ: tassels; Vector: HybridZAP; Site: 1: EcoRI; Site 2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybridZAP. Sample insert size range was 350 bp to 3 kb with a 1 kb average."

ORIGIN

Alignment Scores:

Pred. No.: 5,4e-103 Length: 724
Score: 880.50 Matches: 163
Percent Similarity: 94.30% Conservative: 19
Best Local Similarity: 84.46% Mismatches: 10
Query Match: 88.23% Indels: 1
Gaps: 1

US-10-688-481-11 (1-192) x BQ779008 (1-724)

QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnYsglu 20
Db 43 ATGTTCTGGTGGATCGTCTTATGGGGTCTGCGATCGTTGGCTGTGGCAGAAAGAG 102
QY 21 AlAlaYsIleLeuPheLeuGlyLeuAspAsnAlaGlyYsThrThrLeuLeuHsmetLeu 40
Db 103 GCTAAGATCTCTCTTCTGCTTGCACAGCCGCGAAGACACACCTCTCCATGCTG 162
QY 41 LysAspGluYsLeuGlyGlnHsGlnProThrGlnTyrProThrSerGluLeuSer 60
Db 163 AAGGACAGCGGCTCGTACAGCAGCCAGCGCATATCCCACTGACAGAGTTGAGC 222
QY 61 IleAsnArgValIysPheYsAlaPheAspLeuGlyGlyHsThrIleAlaArgArgVal 80
Db 223 ATCGGAGGATCAAGTTCAGAGGCTTGCAGCTTGGGGCCACAGATCGCCGCGCTC 282
QY 81 TrpArgAspTyrTyrAlaYsValAspAlaIleValYsLeuValAspAlaValAspArg 100
Db 283 TGGAAAGACTACTACGCGCAAGTTGATGCTGTGTGATCTGGTGAAGTGTGACAG 342
QY 101 GluArgPheAlaGluSerIlySlyGluLeuAspSerLeuSerLeuSerAspAspSerLeuSer 120
Db 343 GAAAGTTTGGCGGATCGAAGAGAGAGTGCATCGCTTCTTGCAGATGACTCCCTTGA 402
QY 121 GlnValProValIleuValIleuGlyAsnIysIleAspIleProTyrAlaSerSerGluAsp 140
Db 403 AAGCTTCTTCTTCATACCTGCGCAACAAGATTGACATCCATCGCGGCTTCAGAGAG 462
QY 141 GluLeuArgPheThrLeuGlyLeuThr---MetThrThrGlyYsGlyThrValAsnLeu 159
Db 463 GAGCTGAGGTACTACCTCGCGCTGAGCAACTTCAACCGGGAAGGCAACGTAACTTG 522
QY 160 GluAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgYsMetGly 179
Db 160 GAGCTGAGGTACTACCTCGCGCTGAGCAACTTCAACCGGGAAGGCAACGTAACTTG 522

Db 523 GCCGACTCCAGCTCCGCGCCCTGGAGATCTTCATGTCGATGTGTGGCAGATGGC 582
QY 180 TyrGlyGluGlyPheYsTrpMetThrGlnTyrIleYs 192
Db 583 TATGGCAAGGCTTCNAATGATGATCTCAGTACATCAAG 621

RESULT 9

Bj572166/c
LOCUS
DEFINITION
Bj572166 749 bp mRNA linear EST 18-DEC-2002
CDNA clone jml9003 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Bj572166 749 bp mRNA linear EST 18-DEC-2002
CDNA clone jml9003 3', mRNA sequence.
Bj572166 GI:27253994
EST.
Ipomoea nil (Japanese morning glory)
Ipomoea nil
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Solanales; Convolvulaceae; Ipomoeae; Ipomoea.
1 (bases 1 to 749)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshino@genes.nig.ac.jp.
Location/Qualifiers

FEATURES

source

1. 749
/organism="Ipomoea nil"
/mol_type="mRNA"
/cuiivar="Tokyo-kokei standard"
/db_xref="taxon:35883"
/clone="jml9003"
/tissue_type="mixture of flower and flower bud"
/clone_lib="Ipomoea nil mixture of flower and flower bud"

ORIGIN

Alignment Scores:

Pred. No.: 5,66e-103 Length: 749
Score: 880.50 Matches: 164
Percent Similarity: 94.30% Conservative: 18
Best Local Similarity: 84.97% Mismatches: 10
Query Match: 88.23% Indels: 1
Gaps: 1

US-10-688-481-11 (1-192) x Bj572166 (1-749)

QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnYsglu 20
Db 717 ATGTTCTGGTGGATCGTCTTATGGGGTCTGCGATCGTTGGCTGTGGCAGAAAGAG 658
QY 21 AlAlaYsIleLeuPheLeuGlyLeuAspAsnAlaGlyYsThrThrLeuLeuHsmetLeu 40
Db 657 GCCAAGATCTTGTCTTGGGCTCGCAATGATCGCGGAAACACACTTGTCTCCATATGTTG 598
QY 41 LysAspGluYsLeuGlyGlnHsGlnProThrGlnTyrProThrSerGluLeuSer 60
Db 597 AAGAGTGAAGATTGTTCAACATCAACCAACATATCCCACTGACATCGAGAGCTGAGT 538
QY 61 IleAsnArgValIysPheYsAlaPheAspLeuGlyGlyHsThrIleAlaArgArgVal 80
Db 537 ATTGGCAAAATCAAGTTCAGAGGCTTTCAGCTTGGAGGCGCATCGCTCCCGTGT 478
QY 81 TrpArgAspTyrTyrAlaYsValAspAlaIleValYsLeuValAspAlaValAspArg 100
Db 477 TGGAAAGACTACTATCTAAGTGTGATGCGTGTATTTATTTGATGATGCTTATGATTA 418
QY 101 GluArgPheAlaGluSerIlySlyGluLeuAspSerLeuSerLeuSerAspAspSerLeuSer 120
Db 101 GAGCTGAGGTACTACCTCGCGCTGAGCAACTTCAACCGGGAAGGCAACGTAACTTG 522

Db	417	GAAAGATTGTGGAGATCGAAGAAAAGATGGATGCTCCCTCTCGATATGATCCCTGGCC	358
Qy	121	GLNValProValLeuValIleuGLYAsnLysIleAspIleProCysAlaSerSerGluAsp	140
Db	357	AATGTACCTTTTCTCGATTTTGGCCAAATAGATCGACATCCCATATGCTGCTTGAAAGT	298
Qy	141	GLuleuArgpPheThrIleuGLYLeuThr---MetThrThrGlyIlybGlyThrValAsnLeu	159
Db	297	GAAATGGCTTACCAACATGGGGTTACAGCGATCCACCACTGGCAAGGGCAAGGTAACTG	238
Qy	160	GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgIlybMetGly	179
Db	237	GCAGATTCCAATGATTCGCCCTCTCGAAGGTATTATCATGTCACACATATGTCGCCAAGTGGGT	178
Qy	180	TyrGlyIlybGlyPheLysTrpMetThrGlnTrpIlybLys	192
Db	177	TATGGAGAGGCTTCAAATGGATGTCTCAATATACATAAAG	139

AUTHORS Kim, H., Collura, K., Wisotski, M., Smart, D., Kudrna, D., Muller, C., Rao, K., Haller, K., Wang, R., Soderlund, C., Walbot, V. and Yu, Y.

TITLE Maize full-length cDNA Project

JOURNAL Unpublished (2005)

COMMENT Contact: Yeisoo Yu
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
Email: yeisoo@genome.arizona.edu
Plate: 0066 row: H column: 23.
Location/Qualifiers

FEATURES

source

1. 877
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
/lab_host="DH10B T1 phage resistant"
/clone_id="ZM BFD"
/note="Vector: PCMV-SPORT 6.1, Site 1: EcoRV, Site 2: NotI; Maize full length cDNA library (3530 library) created by Invitrogen from multiple tissues: Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 day aleurone; 4. immature tassels; stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 day whole seed; 11. 12 day endosperm and embryo; 12. 17 day endosperm and embryo. All of the sequenced clones in Maize full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona
(http://www.genome.arizona.edu/orders/)."

ORIGIN

Alignment Scores:

Pred. No.: 7.08e-103 Length: 877
Score: 880.50 Matches: 163
Percent Similarity: 94.30% Conservative: 19
Best Local Similarity: 84.46% Mismatches: 10
Query Match: 88.23% Indels: 1
DB: 8 Gaps: 1

US-10-688-481-11 (1-192) x DR824574 (1-877)

Qy 1 MecheleuValaApTTPPhetYrGlyPheleuAlaserlleglyleuTTPGlnlyGlu 20
Db 128 ATGTTCTGTGGAGCTGTTCTATGCGGTGCTGTCATCGTGGCTGTGGCAAGAG 187
Qy 21 AlAtyslleuPheleuGlyleuAspAanlaaglylsYrThrTrlleuLeuHlMetleu 40
Db 188 GCTAAGATCTCTTCTTGGCTCGACACCCGCGAAGACCACTCTCCATGCTG 247
Qy 41 LysApGlyuYleuGlyGlnHlsglnProThrglnTyrProThrsGrgluGluLeuSer 60
Db 248 AAGGACGAGCGGCTCGTACAGACACGCGGAGTACCCCACTGAGAAAGTTGAGC 307

Qy 61 lIeAsnArVallybSheleYsAlaPheAspLeuGlyGlyHleThrllleAlaArgArVal 80
Db 308 ATCGGAGATCATCAAGTTCAAGGGCTTCGACTTGGGGGCCACCAAGATCCGCCGCCGTC 367
Qy 81 TTPAAGAspTYrTYrAlaYsValaAlaIleValTYrleuValAspAlaValaAaPAG 100
Db 368 TGGAGGACTTACTACCCCAAGGTTGATGCTGTGTACTTGTGTGATCTGTGGACAAG 427
Qy 101 GUArGPhAlaGlyserlyslYsgluLeuAspSerleuLeuSerAspSerleuSer 120
Db 428 GAACGTTTGGCGAGTCGAGAGAGAGGCTTGATGCCCTTTCGACATGATCTCCCTTGA 487
Qy 121 GlnAlProValleuValleuGlyAenlysIleAspIleProTYrAlaSerSergluAaP 140
Db 488 AACGTTCTTCTCTCACTACGCGCAACAGATTGATCCCATACCGCGCTTCAGAGAG 547
Qy 141 GluleuArgPheThrleuGlyleuThr---MetThrThGlylysglyThrValaenleu 159
Db 548 GAGCTGAGGTACTACCTCGCGCTGAGACCACTTCACAAACCGGAGGCAACGGAACCTG 607
Qy 160 GlyAspSerAsnleArgProIleGluValPheMetCysSerIleValArglysmetGly 179
Db 608 GCCGACTCCAAATGTCGGCCCTCGAGATCTTCATGTGAGTGTGGTGGCAAGATGGC 667
Qy 180 TYrGlyGlyGlyPheYsTrpMetThrGlnTYrIleYs 192
Db 668 TATGGGAGAGGCTTCAATGAGATGCTCATCATCAAG 706

RESULT 12

CO443833 903 bp mRNA linear EST 08-JUN-2005
LOCUS MZCU10063007.9 Maize Endosperm cDNA Library Zea mays cDNA, mRNA
DEFINITION sequence.

ACCESSION CO443833
VERSION CO443833.1 GI:67015084
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 903)
Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa, V.E., Jr., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P.

TITLE Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags
JOURNAL Plant Mol. Biol. (2005) In press
COMMENT Contact: Arruda, P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: patricia@unicamp.br.

FEATURES

source

1. 903
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="F-352 near isogenic line"
/db_xref="taxon:4577"
/sex="hermaphrodite"
/tissue_type="endosperm"
/dev_stage="multiple stages (10 to 25 days after pollination, see publication for more information)"
/lab_host="E. coli DH10B"
/clone_id="Zea Endosperm cDNA Library"
/note="Organ: seed. Vector: pSPORT1. Site 1: SalI. Site 2: NotI; Plant Material and RNA Isolation: Field grown maize plants from inbred line F352 were used. Ears were harvested at 10, 15, 20 and 25 days after pollination (DAP). Seeds were cut from the ear and the upper third of the endosperms, containing only endosperm, aleurone and

pericarpal tissues, was removed, frozen in liquid nitrogen and stored at -800 C. Frozen endosperms were pulverized in liquid nitrogen and total RNA was isolated according to the method of Manning (9). Poly(A)+RNA was isolated using Oligotex-dT. cDNA libraries were constructed using Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning Kit as described in Vettore, et al., (2001). The libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs ranging from 500 to 800 bp in size were assigned as short libraries (S10, S15, S20), and cDNAs >800 were assigned as long libraries (L10, L15, M15, M20, L25). Unamplified libraries were plated and individual colonies picked and transferred to 96 well plates containing liquid Circlet Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each cDNA clone were stored at -800 C. Additional information can be found in : Verra, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fiesch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P. (2005) Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags. Plant Molecular Biology (/in press/)"

ORIGIN

Alignment Scores:
Pred. No.: 7.37e-103 Length: 903
Score: 880.50 Matches: 163
Percent Similarity: 94.30% Conservative: 19
Best Local Similarity: 84.46% Mismatches: 10
Query Match: 88.23% Indels: 1
Gaps: 1

US-10-688-481-11 (1-192) x CO443833 (1-903)

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Oy 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnTysGlu 20
Db 124 ATGTTCTGGTGGATGGTCTCTATGGGGTGGTGGATGGCTTGGGCTGTGGCAAGAG 183
Oy 21 AlAlaYsIleLeuPheLeuGlyLeuAspAsnAlaGlyTyrThrThrLeuLeuHsMetLeu 40
Db 184 GCTAAGATCTCTTCTTGGCTCGACCAACCCGCAAGACACCTCTCCATCATGCTG 243
Oy 41 LysAspGlyLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluLeuSer 60
Db 244 AAGGCGAGCGGCTCGTACACACGCGAGCGAGTCCACGCTCAGAAAGATTGAGC 303
Oy 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db 304 ATCGGACGATCAAGTTCAGGCGCTTGGGCGCACCAAGATGCCCGCGCGCTC 363
Oy 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db 364 TGGAAAGCACTACGACCAAGTTGATCTGTGTGCTTGGTGGAGCTGTGGACAG 423
Oy 101 GluArgPheAlaGlySerLysGlyLeuLeuAspSerLeuLeuSerAspAspSerLeuSer 120
Db 424 GAACGTTTGGCGAGTCAAGAGAGCGCTCGATGCGCTTTCGACATGACTCCCTTGA 483
Oy 121 GlnValProValLeuValLeuGlyValAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
Db 484 AACGTTCTTCTCTTACTGTGGCAACAAGATGATCCATTCATGCTTCCAGAGAG 543
Oy 141 GluLeuArgPheThrLeuGlyLeuThr---MetThrThrGlyLysGlyTyrValAsnLeu 159
Db 544 GAGCTGAGGACTACTCGGCTGAGCAATTCACACACCGGAGAGGGCAAGTGAACCTG 603
Oy 160 GlyAspSerAsnLysArgProIleGluValPheMetCysSerIleValArgLysMetGly 179
Db 604 GCCGACTCAACGTCGCGCCCTGGAAGATCTTCATGTGCAAGTGTGTCGCAAGATGGC 663
Oy 180 TyrGlyGluGlyPheLysTyrMetThrGlnTyrIleLys 192
Db 664 TATGGCAAGGCTTCAATGATGTCTCATGATCATCAAG 702

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RESULT 13
AY106333
LOCUS
DEFINITION
Zea mays
PC0096720 mRNA sequence.
AY106333
VERSION
KEYWORDS
HTC.
SOURCE
Zea mays
Zea mays
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
AY106333.1 GI:21209411

REFERENCE
AUTHORS
Gardner, J., Schroeder, S., Polacco, M.L., Sanchez-Villada, H.,
Fang, Z., Morgante, M., Landewe, T., Fengler, K., Ueche, F.,
Hanley, M., Tingey, S., Chou, H., Wang, R., Soderlund, C. and Coe, E.H.
Jr.
Anchoring 9,371 maize expressed sequence tagged unigenes to the
bacterial artificial chromosome contig map by two-dimensional
overgo hybridization
Plant Physiol. 134 (4), 1317-1326 (2004)

REFERENCE
AUTHORS
2 (bases 1 to 1098)
Kainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., White, M.S.,
Arthur, L.W., Hanley, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
Unpublished (2002)
3 (bases 1 to 1098)
Coe, E.H.

COMMENT
JOURNAL
TITLE
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB, www.zmdb.iastate.edu. TIGR,
researching at MSU, maizeMap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schabbe, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.

FEATURES

source
location/Qualifiers
1..1098
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="maizgdb:635515"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Consensus
Library"

/note="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed Dupont contigs; this resource was
assembled by Dupont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"

ORIGIN

Alignment Scores:
Pred. No.: 9.72e-103 Length: 1098
Score: 880.50 Matches: 163
Percent Similarity: 94.30% Conservative: 19
Best Local Similarity: 84.46% Mismatches: 10
Query Match: 88.23% Indels: 1
Gaps: 1

US-10-688-481-11 (1-192) x AY106333 (1-1098)

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Oy 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnTysGlu 20
Db 189 ATGTTCTGGTGGATGGTCTCTATGGGGTGGTGGATGGCTTGGGCTGTGGCAAGAG 248
Oy 21 AlAlaYsIleLeuPheLeuGlyLeuAspAsnAlaGlyTyrThrThrLeuLeuHsMetLeu 40

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Db 249 GCTAAGATCTCTTCTTGGCTTGACCAACCGGCAAGCAACCTCTCCACATGCTG 308
 Qy 41 LysAspGluLysLeuGlyGlnHISGlnProThrGlnTyrProThrSerGluLeuSer 60
 Db 309 AAGGACAGGAGGCTCGTACAGCACACGACCAAGGACGACGTCAGTAAGAGTTGAGC 368
 Qy 61 LLeasnaGValLysPheLysAlaPheAspLeuGlyGlnHISThrIleAlaArgVal 80
 Db 369 ATGGGACGAGATCAAGATTCAAGGGCTTGACCTTGGGGCCACCAAGATCGCCGCGTGC 428
 Qy 81 TTPArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
 Db 429 TGGAAAGACTACTACGCGCAAGGTTGATGCTGTGTACTGTGGTGGATGCTGTGACAA 488
 Qy 101 GlnArgPheAlaGluSerLysGluLeuAspSerLeuSerLeuSerAspAspSerLeuSer 120
 Db 489 GAACGTTTCCGAGATGGAAGAGAGAGCTGATGCGCTTCTTGCAAGTACCTCCCTTGCA 548
 Qy 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
 Db 549 AAGGTCCTTCTTCCATCACTGGGCAACAGATTGACATCCCATRACGCGCTTCAGAGAG 608
 Qy 141 GlnLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyLysGlyThrValAsnLeu 159
 Db 609 GAGCTGAGTACTACTCTCGGCTGAGCACTTCAACCGGAAAGGCAAGTGAACCTTG 668
 Qy 160 GlnAspSerAsnIleArgProIleGluValPheMetCysSerIleValAlaGlyMetGly 179
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 Qy 180 TyrGluGlyPheLysTyrMetThrGlnTyrIleLys 192
 Db 729 TATGGCAAGGCTTCAATGATGTCTCATGATCAATCAAG 767
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 LOCUS CN206979 861 bp mRNA linear EST 30-APR-2004
 DEFINITION Tor739 Gametophyte rehydration library Tortula ruralis cDNA, mRNA
 sequence.
 ACCESSION CN206979
 VERSION CN206979.1 GI:46903710
 KEYWORDS EST.
 SOURCE Tortula ruralis
 ORGANISM Tortula ruralis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida; Dicranidae; Pottilales; Pottilaceae; Tortula.
 REFERENCE
 AUTHORS Oliver,M.J., Dowd,S.E., Zaragosa,J., Mauget,S.A. and Payton,P.R.
 TITLE The rehydration transcriptome of the desiccation-tolerant bryophyte
 Tortula ruralis: transcript classification and analysis
 JOURNAL BMC Genomics 5 (1), 89 (2004)
 PUBMED 15546486
 COMMENT Contact: Oliver Melvin J
 Plant Stress Lab
 USDA-ARS
 3810 4th St. Lubbock, TX 79415, USA
 Tel: 806-749-5860
 Fax: 806-723-5272
 Email: moliver@lbrk.ars.usda.gov
 PCR PRIMERS
 FORWARD: GTTTTCCAGTCAAGAC
 BACKWARD: CAGGAACGCTATGAC.
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 SOURCE Location/Qualifiers
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 Salt; Site_2: NotI"

Pred. No.: 8e-103
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 Query Match: 88.18%
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 Qy 21 AlAlaLysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuHisMetLeu 40
 Db 232 GCCAAATCTCTCTTGGGCTTCGACCAACGGGGCAAGACACGCTCTTCATATCTC 291
 Qy 41 LysAspGluLysLeuGlyGlnHISGlnProThrGlnTyrProThrSerGluLeuSer 60
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 Db 412 TGGAGAGACTATTATCCCAAGGTGATGCCATATGCTTACTGATGAGACCCCTAGACAG 471
 Qy 101 GlnArgPheAlaGluSerLysGluLeuAspSerLeuSerAspAspSerLeuSer 120
 Db 472 GAGAGTTCCAGAGATCGAAGAAAGAGAGCTGACTGTTGTCTCAACGACATCTCTCC 521
 Qy 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
 Db 532 CAAGTCTGTGCTACTGCTGGGAAACAGATGACATCCCGATACGCGCTTCGAGAG 591
 Qy 141 GlnLeuArgPheThrLeuGlyLeuThrMetThrGlyLysGlyThrValAsnLeuGly 160
 Db 592 GAGCTCGGATATCTCTGGGCTGACCATGACCAAGGCGCATAGGACCTGAACTGGGC 651
 Qy 161 AspSerAsnIleArgProIleGluValPheMetCysSerIleValAlaGlyMetGlyTyr 180
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 Qy 181 GlyGluGlyPheLysTyrMetThrGln 189
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 DEFINITION 5207 C08 Fl5 Switchgrass callus cDNA library Panicum virgatum cDNA
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 ACCESSION DN152566
 VERSION DN152566.1 GI:59873417
 KEYWORDS EST.
 SOURCE Panicum virgatum (switchgrass)
 ORGANISM Panicum virgatum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Paniceae; Panicum.
 REFERENCE
 AUTHORS Tobias,C.M., Twigg,P., Hayden,D.M., Fladbeck,M.R., Vivian,L.A.,
 Chow,E.K. and Sarath,G.
 TITLE An EST survey of Switchgrass: a C4 perennial grass
 JOURNAL Unpublished (2005)
 COMMENT Contact: Tobias CM
 Genomics and Gene Discovery Unit
 USDA, Agricultural Research Service, Western Regional Research
 Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 510 559-6172

Fax: 510 559-5818
Email: cecobias@pw.usda.gov
The piped basecalling program was used to call bases and identify the high scoring region using the '-trim alt' and trim out options. Vector sequences have been removed using the program cross_match.
Seq primer: M13 reverse.

FEATURES
source
Location/Qualifiers
1..807

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/cultivar="Kanolw"
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/clone="5207_C08_F15"
/dev_stage="Embryogenic and Nonembryogenic"
/lab_host="E. coli DH5alpha"
/clone_lib="Switchgrass callus cDNA library"
/note="Organ: Callus; Vector: pSPORT1; Site_1: SalI; Site_2: NotI; Callus was established from mature carpogonia of Switchgrass cv. Kanlow and flash frozen in liquid nitrogen. The tissue was cultured by Dan Hayden in the laboratory of CM Tobias. Total RNA and poly(A) RNA were prepared, cDNA synthesized, and directionally ligated into pSPORT1 by Paul Twigg, Biology Department, U. Nebraska Kearney, Kearney, NE. Plasmid DNA preparations and DNA sequencing were performed in the laboratory of CM Tobias."

ORIGIN

Alignment Scores:

Pred. No.: 1.54e-102 Length: 807
Score: 877.50 Matches: 162
Percent Similarity: 94.30% Conservative: 20
Best Local Similarity: 83.94% Mismatches: 10
Query Match: 87.93% Indels: 1
DB: 8 Gaps: 1

US-10-688-481-11 (1-192) x DN152566 (1-807)

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QY 41 LysAspGlyLysLeuGlyGlnHisGlnProthrglnIyrProthrserGluLeuSer 60
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QY 61 IleAsnArgValIysPheLysAlaPheAspLeuGlyGlnIsthrIleAlaArgArgVal 80
DB 273 ATCGCAAGATCAATTCAGGCCCTTCAGCTCGGCGGCCACACAGATGCTCGCGCTC 332
QY 81 TrpArgAspIyrTyrAlaLysValAspAlaIleValIyrLeuValAspAlaIAspArg 100
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QY 101 GluArgPheAlaGlnSerIlyLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
DB 393 GAACGCTTTCGAGTCAAGAGGAGCTGTATGCTCTTTCGACATGACTCACTTGC 452
QY 121 GluValProValLeuValLeuGlyValAsnYsIleAspIleProIyrAlaSerSerGluAsp 140
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DB 513 GAGCTGCGGTACTACTCGGCTGAGCAACTTCACACCGGGAAGGCAACGTGAACCTTG 572
QY 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgIysMetGly 179
DB 573 TCTGACTCCAAATGTTGCGCCCTGAGATCTTCATGTGCAAGTGTGCGCAAGATGGGC 632

QY 180 TyrGlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
DB 633 TACGCGAAGGCTTCAATGATGATGTCATCATCAAG 671

Search completed: December 9, 2005, 03:49:44
Job time : 3751 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 9, 2005, 01:41:52 / Search time 169 Seconds
(without alignments)
2019.478 Million cell updates/sec

Title: US-10-688-481-11
Perfect score: 998
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Delop 6.0, Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	998	100.0	805	3	US-09-828-310-1
3	674.5	67.6	3191	3	US-09-270-767-13105
4	625	62.6	716	3	US-09-533-559-6998
5	614.5	61.6	724	2	US-08-825-780-2
6	614.5	61.6	1228	3	US-09-149-476-285
7	614.5	61.6	1285	3	US-09-149-476-146
8	585.5	58.7	564	3	US-09-248-796A-6222
9	560.5	56.2	903	3	US-09-016-434-913

10	542	54.3	1700	3	US-09-533-559-125	Sequence 125, App
11	386	38.7	378	3	US-09-621-976-458	Sequence 458, App
12	355	35.6	504	3	US-09-621-976-445	Sequence 445, App
13	305	30.7	271	3	US-09-313-294A-3554	Sequence 3554, App
14	282	28.3	262	3	US-09-016-434A-501	Sequence 501, App
15	275.5	27.6	968	3	US-09-949-016-3194	Sequence 3194, App
16	260	26.1	459	3	US-09-270-767-1354	Sequence 1354, App
17	253	25.4	676	3	US-09-533-559-6626	Sequence 1636, A
18	253	25.4	1273	3	US-09-533-559-6704	Sequence 6626, App
19	250.5	25.1	1125	3	US-09-774-528-374	Sequence 6704, App
20	250.5	25.1	1125	3	US-10-120-988-374	Sequence 374, App
21	250.5	25.1	1125	3	US-09-513-999C-10983	Sequence 10983, A
22	248	24.8	587	3	US-09-248-796A-6221	Sequence 6221, App
23	246	24.6	513	3	US-09-463-339-4	Sequence 4, App1
24	245.5	24.6	913	3	US-09-621-976-984	Sequence 984, App
25	243	24.3	540	3	US-09-533-559-111	Sequence 111, App
26	243	24.3	558	3	US-09-248-796A-6161	Sequence 6161, App
27	242.5	24.3	550	3	US-09-359-301A-24	Sequence 24, App1
28	241.5	24.2	550	3	US-09-771-035A-12	Sequence 12, App1
29	241.5	24.2	550	3	US-09-533-559-4366	Sequence 4366, App
30	241	24.1	663	3	US-09-949-016-4833	Sequence 4833, App
31	240.5	24.1	3595	3	US-09-270-767-12090	Sequence 12090, A
32	240	24.0	1076	3	US-09-503-391-5	Sequence 5, App1
33	239	23.9	558	3	US-08-984-550-3	Sequence 3, App1
34	238.5	23.9	536	3	US-09-359-301A-23	Sequence 23, App1
35	238.5	23.9	550	3	US-09-771-035A-11	Sequence 11, App1
36	238.5	23.9	550	3	US-08-984-550-1	Sequence 1, App1
37	238.5	23.9	950	3	US-09-220-132-69	Sequence 69, App1
38	237.5	23.8	1815	3	US-09-949-016-2652	Sequence 2652, App
39	237.5	23.8	1855	3	US-09-949-016-2434	Sequence 2434, App
40	237.5	23.8	1985	3	US-09-949-016-2435	Sequence 2435, App
41	237.5	23.8	2366	3	US-09-513-999C-3820	Sequence 3820, App
42	235.5	23.6	1005	3	US-09-103-359-4	Sequence 4, App1
43	234.5	23.5	271	3	US-09-313-294A-3059	Sequence 3059, App
44	234	23.4	543	3	US-09-248-796A-5795	Sequence 5795, App
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ALIGNMENTS

RESULT 1
US-09-828-310-6
Sequence 6, Application US/09828310
Patent No. 6689939
GENERAL INFORMATION:
APPLICANT: COSTA E SILVA, OSWALDO DA
APPLICANT: BOHNERT, HANS J.
APPLICANT: VAN THIELEN, NOCHA
APPLICANT: CHEN, ROUYING
TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
FILE REFERENCE: 16313-0039
CURRENT APPLICATION NUMBER: US/09/828,310
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/196,001
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 667
TYPE: DNA
ORGANISM: Physcomitrella patens
US-09-828-310-6
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Pred. No.: 5,74e-120
Score: 998.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 3
Gaps: 0
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RESULT 2

US-09-828-310-1/c
; Sequence 1, Application US/09828310
; Patent No. 6689939
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: BOHNER, HANS J.
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
; FILE REFERENCE: 16313-0039
; CURRENT APPLICATION NUMBER: US/09/828,310
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 805
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-09-828-310-1

Alignment Scores:

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Score: 998.00 Matches: 192
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-688-481-11 (1-192) x US-09-828-310-1 (1-805)

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Db 693 GCCAAATCCTGTTCTGGGTCTCGACATGCTGGCAAGACTACTCTTCTGCAATGCTC 634
Qy 41 LysAspGluLysLeuGlyGlnHisGlnProThrGlnTygProThrSerGluLysLeuSer 60
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Db 573 ATCAACAGAGTGAAGTTCAAGCATTCGATCGGTGGCCACACATCGCTCGACGGGTG 514
Qy 81 TrpArgAspTygTygAlaLysValAspAlaIleValTygLeuValAspAlaValAspArg 100
Db 513 TGGAGGAGCTACTATGCTTAAGTGATGCTATAGTATCTCGTCGACGAGTGAACAGG 454
Qy 101 GluArgPheAlaGluSerLysLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
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Qy 121 GlnValProValIleuValIleuGlyAsnLysIleAspIleProTygAlaSerSerGluAsp 140
Db 393 CAAGTTCTGTGCTGCTGCTGGGAAACAGATTGATATCCGTTACGCTTCTGAAAGAC 334
Qy 141 GluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyGlyGlyThrValAsnLeuGly 160
Db 333 GAGTTCGGGTTCACACTGGGTGACCATGACCATGTTAAAGAAACGGTAAACCTGGGA 274
Qy 161 AspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGlyTyg 180
Db 273 GATACCAACATTGGCCCATTTGAGGTTTTCATGTGCATGATATTGGCCAAATGGGGTAC 214
Qy 181 GlyGluGlyPheLysTrpMetThrGlnTygIleLys 192
Db 213 GGTGAAGTTTCAAGTGATGACCCAGTACATCAAG 178

RESULT 3

US-09-270-767-13105
; Sequence 13105, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13105
; LENGTH: 3191
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13105

Alignment Scores:

Pred. No.: 5.5e-77 Length: 3191
Score: 674.50 Matches: 127
Percent Similarity: 79.69% Conservative: 26
Best Local Similarity: 66.15% Mismatches: 38
Query Match: 67.59% Indels: 1
DB: 3 Gaps: 1

US-10-688-481-11 (1-192) x US-09-270-767-13105 (1-3191)

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/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 724 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: BRSTTUM14
/ CLONE: 2742252
/ US-08-825-780-2

Alignment Scores:
Pred. No.: 3,86-70 Length: 724
Score: 614.50 Matches: 115
Percent Similarity: 77.44% Conservative: 36
Best Local Similarity: 58.97% Mismatches: 39
Query Match: 61.57% Indels: 5
DB: 2 Gaps: 3

US-10-688-481-11 (1-192) x US-08-825-780-2 (1-724)
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Qy 78 ArgArgValITTPAAspTYrTYrAlaIysValAspAlaIleValTYrLeuValAspAla 97
Db 299 CGAAGAGGTGAAAGAACTTCTCTGCTATCAATGCGATGATTTCTGTGATTTGT 358
Qy 98 ValAspArgGluIysPheAlaGluSerIysIysGluLeuAspSerIleuSerAspAsp 117
Db 359 GCAGCCACGAAAGGCTGTAGAGTCAAAAGAAAGAACTTGATTCATTAATACAGATCAA 418
Qy 118 SerIysSerGlnValIProValIleuValLeuGlyAsnIysIleAspIleProTYrAlaSer 137
Db 419 ACCATTGCTAAATGTCCTATACTGATCTTGGGAATTAAGATCGACAGACCTGAAGCCATC 478
Qy 138 SerGluAspGluLeuArgPheThrIleuGlyLeu---ThrMetThrThGlyIysGlyThr 156
Db 479 AGTGAAGAGAGGTGCGAGAGATGTTTGTTTAATGTCTCAGACAAACGAGAAAGGGAGT 538
Qy 157 ValAsnLeuGlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArg 176
Db 539 ATATCTCTGAAAGAACTGAATGCCGACCTTGAAGATTTTCATGTGATGTGTCTCAA 598
Qy 177 LysMetGlyTYrGlyGluGlyPheIysThrPheThrGlnTYrIle 191
Db 599 AGACAAAGTTACGAGGAAGGCTTCGCTGATGCGACAGTACATT 643

RESULT 6
US-09-149-476-285
/ Sequence 285, Application US/09149476
/ Patent No. 6420526
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: 186 Human Secreted proteins
/ FILE REFERENCE: P2002PI
/ CURRENT APPLICATION NUMBER: US/09/149,476
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/ CURRENT FILING DATE: 1998-09-08
/ EARLIER APPLICATION NUMBER: PCT/US98/04493
/ EARLIER FILING DATE: 1998-03-06
/ EARLIER APPLICATION NUMBER: 60/040,162
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,333
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/038,621
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,626
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,334
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,336
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,163
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/047,600
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,615
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,597
/ EARLIER FILING DATE: 1997-05-23
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/ EARLIER APPLICATION NUMBER: 60/047,633
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/ EARLIER APPLICATION NUMBER: 60/047,583
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,617
/ EARLIER FILING DATE: 1997-05-23
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/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,592
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,581
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,584
/ EARLIER FILING DATE: 1997-05-23
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/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,587
/ EARLIER FILING DATE: 1997-05-23
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/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,596
/ EARLIER FILING DATE: 1997-05-23
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/ EARLIER FILING DATE: 1997-05-23
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/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,601
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/043,580
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,566
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,314
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/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,311
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,671
/ EARLIER FILING DATE: 1997-04-11
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[illegible]

1	EARLIER FILING DATE: 1997-05-23
2	EARLIER APPLICATION NUMBER: 60/047,594
3	EARLIER FILING DATE: 1997-05-23
4	EARLIER APPLICATION NUMBER: 60/047,599
5	EARLIER FILING DATE: 1997-05-23
6	EARLIER APPLICATION NUMBER: 60/047,593
7	EARLIER FILING DATE: 1997-05-23
8	EARLIER APPLICATION NUMBER: 60/047,614
9	EARLIER FILING DATE: 1997-05-23
10	EARLIER APPLICATION NUMBER: 60/043,578
11	EARLIER FILING DATE: 1997-04-11
12	EARLIER APPLICATION NUMBER: 60/043,576
13	EARLIER FILING DATE: 1997-04-11
14	EARLIER APPLICATION NUMBER: 60/047,501
15	EARLIER FILING DATE: 1997-05-23
16	EARLIER APPLICATION NUMBER: 60/043,670
17	EARLIER FILING DATE: 1997-04-11
18	EARLIER APPLICATION NUMBER: 60/056,632
19	EARLIER FILING DATE: 1997-08-22
20	EARLIER APPLICATION NUMBER: 60/056,664
21	EARLIER FILING DATE: 1997-08-22
22	EARLIER APPLICATION NUMBER: 60/056,876
23	EARLIER FILING DATE: 1997-08-22
24	EARLIER APPLICATION NUMBER: 60/056,881
25	EARLIER FILING DATE: 1997-08-22
26	EARLIER APPLICATION NUMBER: 60/056,909
27	EARLIER FILING DATE: 1997-08-22
28	EARLIER APPLICATION NUMBER: 60/056,875
29	EARLIER FILING DATE: 1997-08-22
30	EARLIER APPLICATION NUMBER: 60/056,863
31	EARLIER FILING DATE: 1997-08-22
32	EARLIER APPLICATION NUMBER: 60/056,887
33	EARLIER FILING DATE: 1997-08-22
34	EARLIER APPLICATION NUMBER: 60/056,908
35	EARLIER FILING DATE: 1997-08-22
36	EARLIER APPLICATION NUMBER: 60/048,964
37	EARLIER FILING DATE: 1997-06-06
38	EARLIER APPLICATION NUMBER: 60/057,653
39	EARLIER FILING DATE: 1997-09-05
40	EARLIER APPLICATION NUMBER: 60/056,884
41	EARLIER FILING DATE: 1997-08-22
42	EARLIER APPLICATION NUMBER: 60/057,665
43	EARLIER FILING DATE: 1997-09-05
44	EARLIER APPLICATION NUMBER: 60/049,610
45	EARLIER FILING DATE: 1997-06-13
46	EARLIER APPLICATION NUMBER: 60/061,060
47	EARLIER FILING DATE: 1997-10-02

Alignment Scores:		
Pred. No.:	8, 266-70	1238
Score:	614.50	Matches: 115
Percent Similarity:	77.44%	Conservative: 36
Best Local Similarity:	56.97%	Mismatches: 39
Query Match:	61.57%	Indels: 3
DB:	3	Gaps: 3

QY 2 pheLeuValaapTnpheTyr---GlyPhe-----LeuAlaSerIleGlyLeuTnp 17
Db 95 TTCAATATTGATTGGATTGATTACAGTGGTTCCACAGCTGTCCTACAGTTTATGGATTATAT 154
QY 18 GlnLysGluAlaLysIleuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeu 37
Db 155 AAGAAAACGTGGTAACCTGGTATTTCTTGATTGGATTGAATACGAGAAAAACAACATTGGCTA 214
QY 38 HisMetLeuLysAspGlnLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGlu 57
Db 215 CACATGCTAAAGAAGATGACAGACACTTGGACAAACATGTCGCCAACATTACATCCCACTCCGAA 274
QY 58 GlnLeuSerIleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAla 77
Db 275 GAACGTACCACTTGTCTGCAGTACGCTTTCACACTTTTGGATCTGGGTGCACACTGTTCAGCT 334

Qy 78 ArgArgValIrrPaGAspTYrTYrAlaIysValAspAlaIleValTYrLeuValAspAla 97
Db 335 CGAAGAGTGTGGAAGAACTACCTCCGCTATCATATGATGCAATGATTTCTGTGTGTGT 394
Qy 98 ValAspArgIuAqPheAlaGluSerIlyeGluLeuAspSerLeuLeuSerAspAsp 117
Db 395 GCAACACCAAGAAAGCTGTAGTCAAGAAAGAACTGTATTCATTAATGCAAGTAA 454
Qy 118 SerLeuSerGluValProValIleuValLeuGluIysIleAspIleProTYrAlaSer 137
Db 455 ACCATGCTAATGTGCTATACCTATCTGGAATTAAGTCAAGACCACTGAAGCCATC 514
Qy 138 SerGluAspGluLeuArgPheThrIleuGlyLeu---ThreMetThrGlyIysGlyThr 156
Db 515 AGTGAAGAGAGCTTGCAGAGATGTTGTTTATATGCTACAGACACAGAAAGGGAGT 574
Qy 157 ValAspLeuGlyAspSerAspIleArgProIleGluValPheMetCysSerIleValArg 176
Db 575 ATATCTCGAAGAACTGAATGCGCCGACCTTAGAAGTTTCAATGTAGTGTCTCAAA 634
Qy 177 LysMetGlyTYrGlyGluGlyPheIysThrMetThrGlnTYrIle 191
Db 635 AGACAAAGGTACGAGAGAGGCTTCGCTGATGCAAGTACAT 679
RESULT 7
US-09-149-476-146
Sequence 146, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002p1
CURRENT APPLICATION NUMBER: US/09/149,476
EARLIER FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,879


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; EARLIER APPLICATION NUMBER: 60/056,804
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Alignment Scores:
Pred. No.:      8,83e-70      Length:      1285
Score:          614.50      Matches:      115
Percent Similarity: 77.44%      Conservative: 36
Best Local Similarity: 58.97%      Mismatches:  39
Query Match:      61.57%      Indels:      5
DB:               3          Gaps:      3

US-10-668-481-11 (1-192) x US-09-149-476-146 (1-1285)

QY      2 PheleuValAspTTPheTyr--GlyPhe-----LeuAlaSerIleGlyLeuTTP 17
Db      122 TTCAATTATTGGATTGGATTATACAGTGGTTTCACACAGTGTCTACAGTTTATAGATTATAT 181

QY      18 GlnlysgGluAlaIyIleleuPheleuGlyLeuAspAspAlaGlylystThrPheLeu 37
Db      182 AAGAAACCTGGTAACTGGTATTTCTGGATTGGATTAAGCAGGAAACAAACATTGCTA 241

QY      38 HisMetLeuLysAspGlyLeuGlyLeuGlyGlnHisGlnProThrGlnTyrProThrSerglu 57
Db      242 CACATGCTAAAGATGACAGACTTGACACAACTGTCCCAACTATACATCCCACTTCCGAA 301

QY      58 GluLeuSerIleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAla 77
Db      302 GAACGACCAATTCCTGCGATCAGCTTACCACTTTGATCTGGTGAGACATGTTCAAGCT 361

QY      78 ArgArgValITTPArgAspTyrTyrAlaLysValAspAlaIleValYrLeuValAspAla 97
Db      362 CGAAGAGGTGGAAACATCACTTCTCTGATCAAGGATGATGATTTCTGGTGATGT 421

QY      98 ValAspArgGluArgPheAlaGlySerLysGlyLeuAspSerLeuSerAspAsp 117
Db      422 GCAGACCCGAAAGGCTGTGAGTCAAAAGAAAGAACTTGATCATTACTAATGACAGATGAA 481

QY      118 SerLeuSerGlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSer 137
Db      482 ACCATTGGTAATGTGCTTATACTGATTTCTGGGAATTAAGTGCAGACCTGAAGCATC 541

QY      138 SerGluAspGluLeuArgPheThrLeuGlyLeu---ThrMetThrThrGlyLysGlyThr 156
Db      542 AGTGAAGAGAGGCTTCGAGAGATGTTGGTTTATATAGTCAGACAAACAGAAAGGGGAGCT 601

QY      157 ValAsnLeuGlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArg 176
Db      602 ATATCTCGAAGAAAGCTGATGATCCGACCCCTTAAGAAAGTTTCAATGATGATGCTGCTAAA 661

QY      177 LysMetGlyTyrGlyGlyGlyPheLysTyrMetThrGlnTyrIle 191
Db      662 AGACAGAGTTACGAGAAAGGCTTCGCTGATGAGCACAATACATT 706

RESULT 8
US-09-248-766A-6222
; Sequence 6222, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409

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; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO 6222
 ; LENGTH: 564
 ; TYPE: DNA
 ; ORGANISM: Candida albicans
 US-09-248-796A-6222

Alignment Scores:	
Pred. No.:	1,539-66
Score:	585.50
Percent Similarity:	77.35%
Best Local Similarity:	62.98%
Query Match:	58.67%
DB:	3
Length:	566
Matches:	11
Conservative:	26
Mismatches:	40
Indels:	1
Gaps:	1

US-10-688-481-11 (1-192) X US-09-248-796A-6222 (1-564)

Oy	11	LeuAlSerIleGlyLeuTrpGlnuYsgValuAluYsIleuPheLeuGlyLeuAspAsn	30
Db	22	TTATCATCATTAAGAGATTATGGAATTAACATGCCAAATTATTTATTTTGGGTTGATAT	81
Oy	31	AlaGlyLysThrThrLeuLeuHisMetLeuLysAspGluLysLeuGlyGlnHisGlnPro	50
Db	82	GCTGGTAAACCTACTCTTTTATCATATGTTAAAGATAGATAGATGGCCACTTTCACCA	141
Oy	51	ThrGlnTyrProThrIserGluGluLeuSerIleAsnArgValLysPheLysAlaPheAsp	70
Db	142	ACATTACATCCAACTTCAGAGAAATTGGCCATTGGATCAGTTAGATTACTACTTTGAT	201
Oy	71	LeuGlyGlyHisThrIleAlaArgArgValTPArgAspTyrTyrAlaLysValAspAla	90
Db	202	TTAGTGGACATCAACACAGCTGACAGATTAATGGAAGAATATTATTCCTCCGAAGTCAATGCT	261
Oy	91	IleValTyrIleValAspAlaValAspArgIuArgPheAlaGluSerLysGluLeu	110
Db	262	ATTGCTCTTTTATGTCAGTCTGCTGCTGATACCGAAAGATTGCTGAAATCCAAAGCTGAATTG	321
Oy	111	AspSerIleuSerLeuSerLeuSerLeuSerGlnValProValLeuValLeuGlyAsnLys	130
Db	322	GAAGATTATTTAGAAATTGCAAGATTAAGATCAAGTTGATATTTTGGTAAATAG	381
Oy	131	IleAspIleProTyrAlaSerSerGluAspGluLeuArgPheThrLeuGlyLeuThrMet	150
Db	382	ATTGATATTTCTCTACTGACAGAGGGGAATGCAATTTGAAAAATATGCCCTTGATTTATATAT	441
Oy	151	ThrThrGlyLysGlyThrValAsnLeuGlyAspSerAsnIleArgProIleGlnValPhe	170
Db	442	ACTACTGGTAAAGACTCGTAAATATTGCCGTAAGGACT---AGACCAATTGAAGTGTTT	498
Oy	171	MetCysSerIleValArgLysMetGlyTyrGlyGluGlyPheLysTyrMetThrGlnTyr	190
Db	499	ATGGTTTCCGTTGTTATGAGATCTGGATATGGTGAAGCCTTCCAAATGGTTATCACAATAC	558
Oy	191	Ile 191	
Db	559	ATT 561	

RESULT 9
US-09-016-434-913
; Sequence 913, Application US/09016434

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA

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1  COUNTRY: USA
2  ZIP: 94304
3  COMPUTER READABLE FORM:
4  MEDIUM TYPE: floppy disk
5  COMPUTER: IBM PC compatible
6  OPERATING SYSTEM: PC-DOS/MS-DOS
7  SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2.2
8  COMMENTS: INFORMATION

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Alignment Scores:	
Pred. No.:	5.35e-63
Score:	560.50
Percent Similarity:	75.13%
Best Local Similarity:	56.35%
Query Match:	56.16%
DB:	3
Length:	903
Matches:	115
Conservative:	37
Mismatches:	42
Indels:	7
Gaps:	3

US-10-688-481-11 (1-192) X US-09-016-434-913 (1-903)

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Oy      2 PheLeuValAspTrpPheTyr---GlyPhe-----LeuAlaSerIleGlyLeuTrp 17
Db      215 TTGATCTTTGAGGATGATTCACAAATGAGCTTCAGCAGTGTGCTCCAGCTTCCTGAGACTGTAC 274

Oy      18 GluAlaSerGluAlaValSerIleuPheLeuGluIleuAspAlaValGlySerThrPheLeu 37
Db      275 AAGAAATCTGGAAGAACTGTATCTTACGTTGGATATATGAGGCAGCAAAACACCTCTT 334

Oy      38 HisMetLeuLysAspGluLysLeuGluGlnHisGlnProThrGlnTyrProThrSerGlu 57
Db      335 CACATGCTCAAGATGACAGATTTGGGCCCAACATGTTCCAACTACATCCGACATCAGAA 394

Oy      58 GluLeuSerIleAsnArgValLysPheLysAlaPheAspLeuGluGlyHisThrIleAla 77
Db      395 GACCTACCAATGCTCGAATGACCTTTCAACTTTGATCTTGGTGGGCAAGACCAAGCA 454

Oy      78 ArgArgValIlePheArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAla 97
Db      455 CGTGGCGTTGGAAAAATATATCTCCACAGCAATTAATGGAATGTGCTTCTTGCTGAGACTGT 514

Oy      98 ValAspArgGluArgPheAlaGluSerLysGluLeuAspSerLeuLeuSerAspAsp 117
Db      515 GCAGATCATCTTCGCGCTCGGTGAATCCAAAGTGAAGCTTAATGCTTAATGATCATGAGAA 574

Oy      118 SerLeuSerGlnValProValLeuValLeuGluGlyAsnLysIleAspIleProTyrAlaSer 137
Db      575 ACAATATCCATATGCCCAATCTTATCTTGCGGTAAACAAATATGACAGAACAGATGACATC 634

Oy      138 SerGluAspGluLeuArgPheThrLeuGlyLeu---ThrMetTrpThrGlyLysGlyThr 156

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Db 635 AGTGAAGAAAACTCCGTGATATTGGCTTATGACAGACCAAGGAAGGGAAT 694
Qy 157 ValAsnLeuGlyAspSerAniLeaGProIleGluValPheMetCysSerIleValArg 176
Db 695 GTGACCCCTGAAGAGCTGAATGCTCCGCCATGAAAGTGTTCATGTGCACTGTGCTCAAG 754
Qy 177 LyMetGlyTyrGlyGlu-GlyPheLeuTpmMet-ThrGlnTyrIle 191
Db 755 AGCGAAGCTTACGGCGAGGGGTTTCCGCTCTTCCCAATATT 801
RESULT 10
US-09-533-559-125
; Sequence 125, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods for Monitoring Multiple Gene
; FILE OF INVENTION: Expression
; FILE REFERENCE: 5849,200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; EARLIER FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 1700
; TYPE: DNA
; ORGANISM: Fusarium venenatum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)-(1700)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-125
Alignment Scores:
Pred. No.: 3,41e-60 Length: 1700
Score: 542.00 Matches: 112
Percent Similarity: 73.85% Conservative: 32
Best Local Similarity: 57.44% Mismatches: 46
Query Match: 54.31% Indels: 6
Gaps: 2
US-10-688-481-11 (1-192) x US-09-533-559-125 (1-1700)
Qy 1 MetPheLeuValAspTyrPheTyrGlyPheLeuAlaSerIleGlyLeuTpmGlnValArg 20
Db 112 ATGTGATGATCTCAAGTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 171
Qy 21 AlAlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyValSerThrLeuLeuHisMetLeu 40
Db 172 GCAGAGGTGCTTTCTCGGTCTTGACACGCGGAAAGACTACTCTTCTCCACATGCTG 231
Qy 41 LyAspGluValLeuGlyGlnHisGlnProThrGlnTyrProThrSerGlnGluLeuSer 60
Db 232 AAGAGACACCGTGTGTCATTTCCAGCCCACTTTCAACCCCACTCCAGAGACCTTGCT 291
Qy 61 IleAsnArgValIleValPheLeuValAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db 292 ATTGTGAAGCTCCGCTTCAACCACTTTCGATCTTGATGATGATGATGATGATGATGATG 351
Qy 81 TrpArgAspTyrTyrAlaValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db 352 TGGGCGATTACTTCCCGCGAGGTCAACGCTGCTCTTCTTCAACGCGCAAGACAC 411
Qy 101 GluArgPheAlaGluSerIleValGluLeuAspSerLeuLeuSerLeuSer 120
Db 412 GAGGATTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 471

Qy 121 GlnValProValLeuValLeuGlyAsnValIleAspIleProTyrAlaSerSerGluAsp 140
Db 472 AAGTTCCTCTTGTCTATCTCTCGGACCAAGATGACCA-CCGATATCCCTCTCCAGAC 530
Qy 141 GluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyValGlyValValLeuLeuGly 160
Db 531 GAAATCGACACCAACTCGGGCTCTACCAACACCGGTAAAGGCAAGGCTCACTT--- 587
Qy 161 AspSerAniLeaGProIleGluValPheMetCysSerIleValAlaArgIleMet-GlyTyr 180
Db 588 ---GAGGCGATCGACCTATTGATGCTTCACTGCTCANTAGTGTGCGCAAGGTTA 644
Qy 180 rGlyGluGlyPheLeuS-----TrpMetThrGlnTyrIleVal 192
Db 645 CGGGAGCNGGTATACCTGTGTTGTCACAGNTAGCTTAAG 687
RESULT 11
US-09-621-976-458
; Sequence 458, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Joberet, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent .pm
; SEQ ID NO 458
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 119..376
; NAME/KEY: misc_feature
; LOCATION: 143,318,332
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-458
Alignment Scores:
Pred. No.: 6,58e-41 Length: 378
Score: 386.00 Matches: 72
Percent Similarity: 89.53% Conservative: 5
Best Local Similarity: 83.72% Mismatches: 9
Query Match: 38.68% Indels: 0
Gaps: 0
US-10-688-481-11 (1-192) x US-09-621-976-458 (1-378)
Qy 1 MetPheLeuValAspTyrPheTyrGlyPheLeuAlaSerIleGlyLeuTpmGlnValArg 20
Db 119 ATGTCTCTGTGATCTGCTTCTATGAGTGTCTATCGTCTTGTGCTGTGCTGCGAAGAG 178
Qy 21 AlAlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyValSerThrLeuLeuHisMetLeu 40
Db 179 GCTAAGATCTCTTCTTGGCTCGACCAAGCGCGGAAAGACCACTCTCCACATGCTG 238
Qy 41 LyAspGluValLeuGlyGlnHisGlnProThrGlnTyrProThrSerGlnGluLeuSer 60
Db 239 AAGGAGAGCGGCTCTTACAGCACCGCAACCGCATACCCCACTGTCAGAAAGATTGAGC 298
Qy 61 IleAsnArgValIleValPheLeuValAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db 299 ATCGGAGATCAAGATTCAAGGCTTTCGACTTGGGGCCACCAAGATCCGCCCGCTC 358
Qy 81 TrpArgAspTyrTyrAla 86
Db 359 TGAAGAGACTACTTCGCC 376

RESULT 12
US-09-621-976-445
Sequence 445, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jodet, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 445
LENGTH: 504
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 141..503
US-09-621-976-445

Alignment Scores:
Pred. No.: 1,06e-36 Length: 504
Score: 355.00 Matches: 68
Percent Similarity: 74.79% Conservative: 21
Best Local Similarity: 57.14% Mismatches: 26
Query Match: 35.57% Indels: 4
DB: 3 Gaps: 2

US-10-688-481-11 (1-192) x US-09-621-976-445 (1-504)

Qy 2 PheLeuValAspTrpPheTyr---GlyPhe-----LeuAlaSerIleGlyLeuTrp 17
Db 147 TTCACTTGTAGATGATGATCAATGCTTCAAGCATGCTCCAGTCTCTAGAGCTGAC 206
Qy 18 GlnLysGluAlaLysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeu 37
Db 207 AAGAAATCGTAAACCTGTATCTTAGCTTGGATATGACAGGCAAAACACTCTTCTT 266
Qy 38 HisMetLeuLysAspGluLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGlu 57
Db 267 CACATGCTCAAGATGAGATGACCTTTACACTTTTGTCTTGTGGCAGAGACGACR 326
Qy 58 GluLeuSerIleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAla 77
Db 327 GAGCTAACATTTGCTGGAAATGACCTTTACACTTTTGTCTTGTGGCAGAGACGACR 386
Qy 78 ArgArgValLysPheAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAla 97
Db 387 CGTGGCGTTTGGAAAAATTAATCTCCACAGCAATTAATGGATTTCTTCTGTGGACTGT 446
Qy 98 ValAspArgGluArgPheAlaGluSerLysGlyLeuAspSerLeuLeuSerAsp 116
Db 447 GCAGATCATCTTCGCTCGTGGAAATCAAGTTGAGCTTAATGCTTAATGACTGAT 503

RESULT 13
US-09-313-294A-3554
Sequence 3554, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Laligudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PU-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 3554
LENGTH: 271

TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700611878H1
NAME/KEY: unsure
LOCATION: 220, 249, 262, 270
OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-3554

Alignment Scores:
Pred. No.: 9.72e-31 Length: 271
Score: 306.00 Matches: 67
Percent Similarity: 84.62% Conservative: 10
Best Local Similarity: 73.63% Mismatches: 12
Query Match: 30.66% Indels: 4
DB: 3 Gaps: 1

US-10-688-481-11 (1-192) x US-09-313-294A-3554 (1-271)

Qy 102 ArgPheAlaGluSerLysGlyLeuAspSerLeuSerAspAspSerLeuSerGln 121
Db 1 CGATTGCTGATCAAAAAAGAGCTGACGCTCTCTGTCAGATGATCTCTTGGCAAT 60
Qy 122 ValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAspGlu 141
Db 61 GTTCATTTCTCATCTTCTGGCAACAGATTGATATCCGATGCTGCTCTGAAGAGAG 120
Qy 142 LeuArgPheThrLeuGlyLeuThr---MetThrGlyLysGlyThrValAsn-LeuGlu 160
Db 121 CTGGGATACCTCAAGGCTTTAGCACTTCAACACGGAGAGGCAAGGTCAACTTGGG 180
Qy 160 YAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGlyTyr 180
Db 181 CGATTCGAATGTCGGACCACTGAGGT-TTCATGTGAT-GNISTGCAAGATGGGGCT 238
Qy 180 rGlyGluGlyPheLysTrpMetThrGlnTyr 190
Db 239 AGCGATGATNTCAAGTGGGGCTTCCCAATAC 269

RESULT 14
US-09-016-434-501
Sequence 501, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0002 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 501:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 262 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: PROSNON01
 CLONE: 2278736
 US-09-016-434-501

Alignment Scores:
 Pred. No.: 1.2e-27 Length: 262
 Score: 282.00 Matches: 52
 Percent Similarity: 79.76% Conservative: 15
 Best Local Similarity: 61.90% Mismatches: 17
 Query Match: 28.26% Indels: 0
 DB: 3 Gaps: 0

US-10-688-481-11 (1-192) x US-09-016-434-501 (1-262)

QY 11 LeuAlaSerIleGlyLeuTrpGlnLysGluAlaLysIleuPheLeuGlyLeuAspAsn 30
 DB 11 CTACAGTTTATGATTAATAGAAAACTGTAACTGATTTCTTGATGGATTAAT 70
 QY 31 AlAGLYeThrThrLeuLeuHisMetLeuLysAspGluLysLeuGlyGlnHisGlnPro 50
 DB 71 GCAGGAAAAACAACATTGCTACACATGCTAAAGATACAGACTGGACAACATGCCA 130
 QY 51 ThGInTrProThrSerGluGluLeuSerIleHisnArgValLysPheLysAlaPheAsp 70
 DB 131 ACATTACATCCCACTCCGAAGAACTGACCATTTGCTGCATGACGTTACAACTTTGAT 190
 QY 71 LeuGlyGlyHisThrIleAlaArgArgValTrpArgAspTrpTrpAlaLysValAspAla 90
 DB 191 CTGGGGGACATGTTCAAGCTCGAAGAGTGTGGAAAACTACCTCTGCTATCAATGGC 250
 QY 91 IleValTrpLeu 94
 DB 251 ATTGTATTCTG 262

RESULT 15
 US-09-949-016-3194
 ; Sequence 3194, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE REFERENCE: CLO01307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3194
 ; LENGTH: 968
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-3194

Alignment Scores:
 Pred. No.: 5.73e-26 Length: 968
 Score: 275.50 Matches: 64

Percent Similarity: 53.93% Conservative: 39
 Best Local Similarity: 33.51% Mismatches: 77
 Query Match: 27.61% Indels: 11
 DB: 3 Gaps: 2

US-10-688-481-11 (1-192) x US-09-949-016-3194 (1-968)

QY 2 PheLeuValAspTrpPheTrpGlyPheLeuAlaSerIleGlyLeuTrpGlnLysGluAla 21
 DB 100 TTCATATGAGGAGGCTTTTCTTCAAGTATATTTTCCAGTCTGTTGGAACTCGGAAATG 159
 QY 22 LysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHisMetLeuLys 41
 DB 160 AGAATTTTAATTTGGATTTAGTGAAGCAGGAAAAACCAATTTTGTACAGATTACAA 219
 QY 42 AspGluLysLeuGlyGlnHisGlnProThrGlnTrpProThrSerGluLysSerIle 61
 DB 220 GTGGGAAAGTTGTTACTACTATACCTACCATTTGATTTAATGTAGACGGTGACGTAC 279
 QY 62 AsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgArgValTrp 81
 DB 280 AAAAACCTTAATTCAGAGCTGGGATTTAGAGGACAGACAGATTCAGGCCATCTGG 339
 QY 82 ArgAspTrpTrpAlaLysValAspAlaIleValTrpLeuValAspAlaValAspArgGlu 101
 DB 340 AGATGTTACTATTCAACAACAGATGACGATCATTTATGTAGTACAGTTGTGACCGAGAC 399
 QY 102 ArgPheAlaGlnSerLysLysGluLeuAspSerLeuLeuSerAspAspSerLeuSerGln 121
 DB 400 CGAATTGGCATTTCCAAATCAGAGTTAGTTAGTCCATGTTGGAGGAGAGAGCTGAGAAAA 459
 QY 122 ValProValLeuValLeuGlyAsnLysIleAspIleProTrpAlaSerSerGluAspGlu 141
 DB 460 GCCATTTAGTGGTGTGTTGCAATTAACAGACATGAAACAGCCATGACTTCTCAGAG 519
 QY 142 LeuArgPheThrLeuGlyLeuThrMetThrGlyLysGlyThrValAsnLeuGlyAsp 161
 DB 520 ATGGCAAAATTCACCTTGGTTACCTGCC-----TTGAAGGAC 555
 QY 162 SerAsnIleArgProIleGluValPheMetCysSerIleValaArgLysMetGlyTrpGly 181
 DB 556 -----CGAAATGAGCAGATATTCAAAACGTCAGCAACCAAGCACCAGCCTTGAT 606
 QY 182 GluGlyPheLysTrpMetThrGlnTrpLys 192
 DB 607 GAGCAATGGAATGGCAATTGAAACATTAATAA 639

Search completed: December 9, 2005, 03:52:43
 Job time : 173 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 9, 2005, 01:42:26 ; Search time 792 Seconds
(without alignments)
2004.698 Million cell updates/sec

Title: US-10-688-481-11
Perfect score: 998
Sequence: 1 MFVLVDFWFGFLASIGLWKE.....SIVRKMGYGGFKMTQYIK 192

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published Applications NA Main -OPMT=faastap -SUFFIX=p2n.rnpbm
-MIMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1
-MATRIX=blomsu62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptco -NORM=ext
-HEAPSIZE=500 -MNLN=0 -MAXLEN=2000000000
-USRR=US10688481 @CGN 1.1 1549 @runat_05122005_094813_15905 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications_NA_Main: *
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2: /cg2_6/ptodata/1/pubpna/US08_PUBCOMB.seq: *
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8: /cg2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq: *
9: /cg2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq: *
10: /cg2_6/ptodata/1/pubpna/US11_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	998	100.0	667	3	US-09-828-310-6 Sequence 6, Appli
2	998	100.0	667	8	US-10-688-481-6 Sequence 6, Appli
3	998	100.0	805	3	US-09-828-310-1 Sequence 1, Appli
4	998	100.0	805	8	US-10-688-481-1 Sequence 1, Appli
5	880.5	88.2	955	7	US-10-425-114-21639 Sequence 21639, A
6	880.5	88.2	966	7	US-10-425-114-13536 Sequence 13536, A
7	880.5	88.2	1017	7	US-10-425-114-33380 Sequence 33380, A

8	880.5	88.2	1070	8	US-10-425-115-98353 Sequence 98353, A
9	880.5	88.2	1334	8	US-10-425-115-98354 Sequence 98354, A
10	877.5	87.9	954	7	US-10-767-701-13805 Sequence 13805, A
11	872.5	87.4	1184	7	US-10-437-963-45082 Sequence 45082, A
12	867.5	86.9	1164	7	US-10-425-114-26805 Sequence 26805, A
13	864.5	86.6	1047	8	US-10-767-795-1394 Sequence 1394, Ap
14	862.5	86.4	928	7	US-10-767-701-15389 Sequence 15389, A
15	862.5	86.4	968	7	US-10-425-114-20345 Sequence 20345, A
16	862.5	86.4	991	7	US-10-424-599-13515 Sequence 13515, A
17	862.5	86.4	998	7	US-10-425-114-7242 Sequence 7242, Ap
18	862.5	86.4	1051	7	US-10-425-114-20291 Sequence 20291, A
19	862.5	86.4	1073	7	US-10-425-114-378 Sequence 378, App
20	862.5	86.4	1117	7	US-10-425-114-27102 Sequence 27102, A
21	862.5	86.4	1221	8	US-10-425-115-143342 Sequence 143342, A
22	862.5	86.4	1337	8	US-10-425-115-143340 Sequence 143340, A
23	862.5	86.4	1645	8	US-10-425-115-143343 Sequence 143343, A
24	859.5	86.1	1198	7	US-10-425-114-11886 Sequence 11886, A
25	859.5	86.1	1328	7	US-10-424-599-13513 Sequence 13513, A
26	856.5	85.8	1036	7	US-10-424-599-3196 Sequence 3196, A
27	856.5	85.8	1191	7	US-10-424-599-39806 Sequence 39806, A
28	853.5	85.5	807	8	US-10-767-795-1302 Sequence 1302, Ap
29	852.5	85.4	1688	7	US-10-437-963-58939 Sequence 58939, A
30	843.5	84.5	1164	7	US-10-424-599-32367 Sequence 32367, A
31	842.5	84.4	994	8	US-10-767-795-1303 Sequence 1303, Ap
32	836.5	83.8	764	7	US-10-424-599-32368 Sequence 32368, A
33	833.5	83.7	1303	8	US-10-425-115-143338 Sequence 143338, A
34	823.5	82.5	675	3	US-09-770-149-379 Sequence 379, App
35	820.5	82.2	954	7	US-10-437-963-45083 Sequence 45083, A
36	815.5	81.7	532	7	US-10-021-323-15172 Sequence 15172, A
37	768.5	77.0	1066	7	US-10-424-599-142530 Sequence 142530, A
38	758	76.0	660	7	US-10-437-963-20654 Sequence 20654, A
39	744.5	74.6	811	8	US-10-425-115-140995 Sequence 140995, A
40	725.5	72.7	569	7	US-10-021-323-3674 Sequence 3674, Ap
41	698.5	70.0	603	7	US-10-021-323-11457 Sequence 11457, A
42	674.5	67.6	992	10	US-11-097-114-15608 Sequence 15608, A
43	665.5	66.7	570	8	US-10-425-115-12354 Sequence 12354, A
44	627	62.8	570	5	US-10-128-714-2426 Sequence 2426, Ap
45	625	62.6	716	8	US-10-653-047-6998 Sequence 6998, Ap

ALIGNMENTS

RESULT 1
US-09-828-310-6
; Sequence 6, Application US/09828310
; Patent No. US2002006124A1
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: BOHNET, HANS J.
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
; FILE REFERENCE: 16313-0039
; CURRENT APPLICATION NUMBER: US/09/828,310
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 667
; TYPE: DNA
; ORGANISM: Phycocytella patens
; US-09-828-310-6

Alignment Scores:
Pred. No.: 1,08e-116
Score: 998.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 3
Length: 667
Matches: 192
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-688-481-11 (1-192) x US-09-828-310-6 (1-667)

Qy 1 MePheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnLysGlu 20
Db 33 ATGTTCTTGTAAGTATGGTTTACGGCTTTCTTCCAGCATAGGGCTGTGGCAAGAGAG 92

Qy 21 AlaLysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHISmetLeu 40
Db 93 GCCAAATCCGTTCTGGGCTCGACAAATGCTGGCAAGACTACTCTTCTGCACATGCTC 152

Qy 41 LysAspGluLysLeuGlyGlnHISGlnProThrGlnTyrProThrSerGluGluLeuSer 60
Db 153 AAGGATGAGAACTGGGGCAACATCAACCAACGATATCCAAAGTCAGAGAGTTGAGT 212

Qy 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHISThrIleAlaArgVal 80
Db 213 ATCAACAGAGTGAAGTTCAAGCATTCGATCTGGGTGGCCACAAATCGCTCCAGCGCTG 272

Qy 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db 273 TGGAGGGACTACTATGCTAAGTGATGCTATGATGATCTCGTCCAGCGAGTACAGG 332

Qy 101 GluArgPheAlaGluSerLysLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
Db 333 GAGAGATTGCTGAGTCAAGAAAGAGCTCGATTCTCTCTCCGACGATTCTGTCTCC 392

Qy 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
Db 393 CAAGTCTCTGTGCTCGTCTCGGAAACAAAGATTGATATCCGTAACGCTTCTTGAAGAC 452

Qy 141 GluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyLysGlyThrValAsnLeuGly 160
Db 453 GAGTTGGGTTCAACACTGGGTGACCATGACCATGGTAAAGAACGGTGAACCTGGGA 512

Qy 161 AspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGlyTyr 180
Db 513 GATAGCAACATTCGGCCATGAGGTTTTCATGTGCAGTATGTGGCCAAATGGGGTAC 572

Qy 181 GlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
Db 573 GGTGAAGGTTCAAGTGATGATACCCAGTACATCAAG 608

RESULT 2

US-10-688-481-6

Sequence 6, Application US/10688481

Publication No. US20040194163A1

GENERAL INFORMATION:

APPLICANT: COSTA E SILVA, OSWALDO DA

APPLICANT: BOHNERT, HANS J.

APPLICANT: VAN THIELEN, NOCHA

APPLICANT: CHEN, ROUYING

TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE

TITLE OF INVENTION: IN PLANTS

FILE REFERENCE: 16313-0039

CURRENT APPLICATION NUMBER: US/10/688,481

CURRENT FILING DATE: 2003-10-17

PRIOR APPLICATION NUMBER: 60/196,001

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 50

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 6

LENGTH: 667

TYPE: DNA

ORGANISM: Physcomitrella patens

US-10-688-481-6

Alignment Scores:

Pred. No.: 1,08e-116 Length: 667

Score: 998.00 Matches: 192

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 8 Gaps: 0

US-10-688-481-11 (1-192) x US-10-688-481-6 (1-667)

Qy 1 MePheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnLysGlu 20
Db 33 ATGTTCTTGTAAGTATGGTTTACGGCTTTCTTCCAGCATAGGGCTGTGGCAAGAGAG 92

Qy 21 AlaLysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHISmetLeu 40
Db 93 GCCAAATCCGTTCTGGGCTCGACAAATGCTGGCAAGACTACTCTTCTGCACATGCTC 152

Qy 41 LysAspGluLysLeuGlyGlnHISGlnProThrGlnTyrProThrSerGluGluLeuSer 60
Db 153 AAGGATGAGAACTGGGGCAACATCAACCAACGATATCCAAAGTCAGAGAGTTGAGT 212

Qy 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHISThrIleAlaArgVal 80
Db 213 ATCAACAGAGTGAAGTTCAAGCATTCGATCTGGGTGGCCACAAATCGCTCCAGCGCTG 272

Qy 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db 273 TGGAGGGACTACTATGCTAAGTGATGCTATGATGATCTCGTCCAGCGAGTACAGG 332

Qy 101 GluArgPheAlaGluSerLysLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
Db 333 GAGAGATTGCTGAGTCAAGAAAGAGCTCGATTCTCTCTCCGACGATTCTGTCTCC 392

Qy 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
Db 393 CAAGTCTCTGTGCTCGTCTCGGAAACAAAGATTGATATCCGTAACGCTTCTTGAAGAC 452

Qy 141 GluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyLysGlyThrValAsnLeuGly 160
Db 453 GAGTTGGGTTCAACACTGGGTGACCATGACCATGGTAAAGAACGGTGAACCTGGGA 512

Qy 161 AspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGlyTyr 180
Db 513 GATAGCAACATTCGGCCATGAGGTTTTCATGTGCAGTATGTGGCCAAATGGGGTAC 572

Qy 181 GlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
Db 573 GGTGAAGGTTCAAGTGATGATACCCAGTACATCAAG 608

RESULT 3

US-09-828-310-1/c

Sequence 1, Application US/09828310

Patent No. US20020066124A1

GENERAL INFORMATION:

APPLICANT: COSTA E SILVA, OSWALDO DA

APPLICANT: BOHNERT, HANS J.

APPLICANT: VAN THIELEN, NOCHA

APPLICANT: CHEN, ROUYING

TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE

TITLE OF INVENTION: IN PLANTS

FILE REFERENCE: 16313-0039

CURRENT APPLICATION NUMBER: US/09/828,310

CURRENT FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: 60/196,001

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 50

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 805

TYPE: DNA

ORGANISM: Physcomitrella patens

US-09-828-310-1

Alignment Scores:

Pred. No.: 1,42e-116 Length: 805

Score: 998.00 Matches: 192

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-688-481-11 (1-192) x US-09-828-310-1 (1-805)

QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnYsgIu 20
DB 753 ATGTTTCTTGTAAGATTGGTTTACGGCTTTCTTGCGAGCATAGGGCTGTGGCAGAAGAG 694
QY 21 AlAlvSIIleuPheLeuGlyLeuAspAsnAlaGlyIvSthrlleuLeuHISmetLeu 40
DB 693 GCCAAATCTCTGTTCTGGGTCTCGACAAATGCTGGCAAGACTACTCTTCTGCAATGCTC 634
QY 41 LysAspGluLysLeuGlyGlnHISgInProThrGlnTyrProThrSerGlnGluLeuSer 60
DB 633 AAGGATGAGAACTGGGGCAACATCAACCAACGATATCCAGTCGTACAGAGAGTTGAAGT 574
QY 61 IleAsnArgValIlySphelysAlaPheAspLeuGlyGlyHISthrlleuAlaArgArgVal 80
DB 573 ATCAACAGAGTGAAGTTCAAAAGCATTGATCTGGGTGGCCACACATCGCTGACCGCG 514
QY 81 TrpArgAspTyrTyrAlaIysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
DB 513 TGGAGGACTACTATGCTAAAGTGAATGCTATAGTGTATCTCGTCCAGCAGTACAGAG 454
QY 101 GluArgPheAlaGluSerIlySgIuLeuAspSerLeuSerAspAspSerLeuSer 120
DB 453 GAGAGATTGCTGAGTCAAAAGAAAGAGCTGATCTCTCTCCGACGATTCCTGTGCC 394
QY 121 GlnValProValIleuValIleuGlyAsnIlySleAspIleProTyrAlaSerSerGluAsp 140
DB 393 CAAGTTCCTGTGCTGCTGCTCGGGAACACAGATTGATATCCCGTACGCTTCTGAAAGC 334
QY 141 GluLeuArgPheThrIleuGlyLeuThrMetThrThrGlyIysGlyThrValAsnLeuGly 160
DB 333 GAGTTGCGGTTCACACTTGGGTGACCATGACCACTGTTAAAGAAACGGTGAACCTGGGA 274
QY 161 AspSerAsnIleArgProIleGluValPheMetCysSerIleValArgIysMetGlyTyr 180
DB 273 GATAGCAACATTCGGCCCATTTGAGGTTTCATGTGCATATTTGGCCAAATGGGGTAC 214
QY 181 GlyGluGlyPheIlySthrlleuTrpMetThrGlnTyrIleIys 192
DB 213 GGTGAAGGTTTCAAGTGAATGACCCAGTACATCAAG 178

RESULT 4

US-10-688-481-1/c
; Sequence 1, Application US/10688481
; Publication No. US20040194163A1
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: BOHNER, HANS J.
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
; FILE REFERENCE: 16313-0039
; CURRENT APPLICATION NUMBER: US/10/688,481
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/196,001
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 805
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-10-688-481-1

Alignment Scores:
Pred. No.: 1,42e-116 Length: 805
Score: 998.00 Matches: 192
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-10-688-481-11 (1-192) x US-10-688-481-1 (1-805)

QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnYsgIu 20
DB 753 ATGTTTCTTGTAAGATTGGTTTACGGCTTTCTTGCGAGCATAGGGCTGTGGCAGAAGAG 694
QY 21 AlAlvSIIleuPheLeuGlyLeuAspAsnAlaGlyIvSthrlleuLeuHISmetLeu 40
DB 693 GCCAAATCTCTGTTCTGGGTCTCGACAAATGCTGGCAAGACTACTCTTCTGCAATGCTC 634
QY 41 LysAspGluLysLeuGlyGlnHISgInProThrGlnTyrProThrSerGlnGluLeuSer 60
DB 633 AAGGATGAGAACTGGGGCAACATCAACCAACGATATCCAGTCGTACAGAGAGTTGAAGT 574
QY 61 IleAsnArgValIlySphelysAlaPheAspLeuGlyGlyHISthrlleuAlaArgArgVal 80
DB 573 ATCAACAGAGTGAAGTTCAAAAGCATTGATCTGGGTGGCCACACATCGCTGACCGCG 514
QY 81 TrpArgAspTyrTyrAlaIysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
DB 513 TGGAGGACTACTATGCTAAAGTGAATGCTATAGTGTATCTCGTCCAGCAGTACAGAG 454
QY 101 GluArgPheAlaGluSerIlySgIuLeuAspSerLeuSerAspAspSerLeuSer 120
DB 453 GAGAGATTGCTGAGTCAAAAGAAAGAGCTGATCTCTCTCCGACGATTCCTGTGCC 394
QY 121 GlnValProValIleuValIleuGlyAsnIlySleAspIleProTyrAlaSerSerGluAsp 140
DB 393 CAAGTTCCTGTGCTGCTGCTCGGGAACACAGATTGATATCCCGTACGCTTCTGAAAGC 334
QY 141 GluLeuArgPheThrIleuGlyLeuThrMetThrThrGlyIysGlyThrValAsnLeuGly 160
DB 333 GAGTTGCGGTTCACACTTGGGTGACCATGACCACTGTTAAAGAAACGGTGAACCTGGGA 274
QY 161 AspSerAsnIleArgProIleGluValPheMetCysSerIleValArgIysMetGlyTyr 180
DB 273 GATAGCAACATTCGGCCCATTTGAGGTTTCATGTGCATATTTGGCCAAATGGGGTAC 214
QY 181 GlyGluGlyPheIlySthrlleuTrpMetThrGlnTyrIleIys 192
DB 213 GGTGAAGGTTTCAAGTGAATGACCCAGTACATCAAG 178

RESULT 5

US-10-425-114-21639
; Sequence 21639, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 21639
; LENGTH: 955
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3354-056-D12_FLI
US-10-425-114-21639

Alignment Scores:
Pred. No.: 1.65e-101 Length: 955

Score: 880.50 Matches: 163
Percent Similarity: 94.30% Conservative: 19
Best Local Similarity: 84.46% Mismatches: 10
Query Match: 88.23% Indels: 1
Gaps: 1

US-10-688-481-11 (1-192) x US-10-425-114-21639 (1-955)

```
QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnLysGlu 20
    |||
Db 98 ATGTTCTGCTGGAGCTGCTGCTCTATGGGGTGTGCTGATCGCTTGGCTGGCAAGAG 157
QY 21 AlaIysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHISmetLeu 40
    |||
Db 158 GCTAAGATCCTCTTCTGGCTTGGCTTGCACAAAGCCGGCAAGACCCCTCCATCATCTG 217
QY 41 LysAspGluLysLeuGlyGlnHISGlnProThrGlnTyrProThrSerGluGluLeuSer 60
    |||
Db 218 AAGGACGAGCGGCTCTGACAGCACAGCCAGACGATGCCACCTCCAGAGAGTTGAGC 277
QY 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyIleThrIleAlaArgArgVal 80
    |||
Db 278 ATCGGACGATCAAGATTCAGAGCGCTTGCACCTTGGGGGCCACAGATCGCCCGCGCTC 337
QY 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
    |||
Db 338 TGGAGAGCTACTACCGCCAGAGTTGATGCTGTGTGACTTGTGTGATGCTGTGTGAG 397
QY 101 GluArgPheAlaGluSerLysLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
    |||
Db 398 GAACGTTTGGCCGATCGCAAGAGAGAGCTGCATGCGCTTCTTGCAGATGACTCCCTTGA 457
QY 121 GlnValProValLeuValLeuGlyLysAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
    |||
Db 458 AACGTTCTCTTCTCATCTACTGGGCAACAGATTGACATCCCATACGCGCTTCAAGAG 517
QY 141 GluLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyLysGlyThrValAsnLeu 159
    |||
Db 518 GAGTGTAGGTACTACTCTCGGCTGAGCAACTTCAACCGGGAAGGGCAAGCTGAACCTTG 577
QY 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGly 179
    |||
Db 578 GCCGACTCCAAAGTCCGCCCCCTGAGAGTCTTCAATGTCATGTCGCGCAAGATGGC 637
QY 180 TyrGlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
    |||
Db 638 TATGGCGAAGGCTTCAATGATGTCTCATGATCAATCAAG 676
```

RESULT 6

US-10-425-114-13536
Sequence 13536, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 13536
LENGTH: 966
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LTB143-001-F4_FLI
US-10-425-114-13536

Alignment Scores:
Pred. No.: 1,688-101 Length: 966
Score: 880.50 Matches: 163
Percent Similarity: 94.30% Conservative: 19
Best Local Similarity: 84.46% Mismatches: 10
Query Match: 88.23% Indels: 1
Gaps: 1

US-10-688-481-11 (1-192) x US-10-425-114-13536 (1-966)

```
QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnLysGlu 20
    |||
Db 130 ATGTTCTGCTGGAGCTGCTGCTCTATGGGGTGTGCTGATCGCTTGGCTGGCAAGAG 189
QY 21 AlaIysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHISmetLeu 40
    |||
Db 190 GCTAAGATCCTCTTCTGGCTTGCACAAAGCCGGCAAGACCCCTCCATCATCTG 249
QY 41 LysAspGluLysLeuGlyGlnHISGlnProThrGlnTyrProThrSerGluGluLeuSer 60
    |||
Db 250 AAGGACGAGCGGCTCTGACAGCACAGCCAGACGATGCCACCTCCAGAGAGTTGAGC 309
QY 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyIleThrIleAlaArgArgVal 80
    |||
Db 310 ATCGGACGATCAAGATTCAGAGCGCTTGCACCTTGGGGGCCACAGATCGCCCGCGCTC 369
QY 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
    |||
Db 370 TGGAGAGCTACTACCGCCAGAGTTGATGCTGTGTGACTTGTGTGATGCTGTGTGAG 429
QY 101 GluArgPheAlaGluSerLysLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
    |||
Db 430 GAACGTTTGGCCGATCGCAAGAGAGAGCTGCATGCGCTTCTTGCAGATGACTCCCTTGA 489
QY 121 GlnValProValLeuValLeuGlyLysAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
    |||
Db 490 AACGTTCTCTTCTCATCTACTGGGCAACAGATTGACATCCCATACGCGCTTCAAGAG 549
QY 141 GluLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyLysGlyThrValAsnLeu 159
    |||
Db 550 GAGTGTAGGTACTACTCTCGGCTGAGCAACTTCAACCGGGAAGGGCAAGCTGAACCTTG 609
QY 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGly 179
    |||
Db 610 GCCGACTCCAAAGTCCGCCCCCTGAGAGTCTTCAATGTCATGTCGCGCAAGATGGC 669
QY 180 TyrGlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
    |||
Db 670 TATGGCGAAGGCTTCAATGATGTCTCATGATCAATCAAG 708
```

RESULT 7

US-10-425-114-33380
Sequence 33380, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 33380
LENGTH: 1017
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: UC-ZMFLMO17103E09_FLI

US-10-425-114-33380

Alignment Scores:

Pred. No.:	1,8e-101	Length:	1017
Score:	880.50	Matches:	163
Percent Similarity:	94.30%	Conservative:	19
Best Local Similarity:	84.46%	Mismatches:	10
Query Match:	88.23%	Indels:	1
DB:	7	Gaps:	1

US-10-688-481-11 (1-192) x US-10-425-114-33380 (1-1017)

```
Qy 1 MetPheLeuValAspTrpPheTYRGLYPheLeuAlaSerIleGlyLeuTrpGlnYsglu 20
Db 111 ATGTCTCGTGGACCTGCTTCTATGGGCTGCTGGCATCGCTTGGGCTGTGGCAAGAG 170
Qy 21 AlAlysIleLeuPheLeuGlyLeuAspAsnAlaGlyYsThrThrLeuLeuHISmetLeu 40
Db 171 GCTAAGATCCTCTCTCTGCTGCTGCAACGCGGCAAGACCACTCTTCACATGCTG 230
Qy 41 LysAspGluLysLeuGlyGlnHisGlnProThrGlnTrpProThrSerGluLeuSer 60
Db 231 AAGGACGAGCGGCTGTCAGACACGACGACGACGACGACGACGACGACGACGACGACG 290
Qy 61 IleAsnArgValIysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db 291 ATCGGACGATCAAGTTCAAGCGCTTGAACCTTGGGGCCACAGATCGCCCGCGCTC 350
Qy 81 TrpArgAspTrpTYRAlaLysValAspAlaIleValTYRLeuValAspAlaValAspArg 100
Db 351 TGGAGAGACTACTACGCGCAAGGTTGATGCTGTGTGTACTTGGTGTGATGCTGTGACAAG 410
Qy 101 GluArgPheAlaGlnSerIleYsgluLeuAspSerLeuSerAspAspSerLeuSer 120
Db 411 GAACGTTTCCGAGTCGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 470
Qy 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTYRAlaSerSerGluAsp 140
Db 471 AAGTTCCTTCTCTCACTGCGGCAACAGATTGACATCCCATACGCGGCTTCAGAGAG 530
Qy 141 GluLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyLysGlyThrValAsnLeu 159
Db 531 GAGCTGAGTACTACCTCGGCTGAGCACTTCACACCGGGAAGGCAAGTGAACCTTG 590
Qy 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValAlaGlyMetGly 179
Db 591 GCGGACTCCCATATGTCGCGCCCTGAGAGATCTTCATGTGAGTGTGGCCCAAGATGGGC 650
Qy 180 TYRGLYGLUGLYPHELYSTRPMETTRHGINTRYILEYS 192
Db 651 TATGGCGAAGGCTTCAATGATGATCTCAGTACATCAAG 689

RESULT 8
US-10-425-115-98353
; Sequence 98353, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425, 115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 98353
; LENGTH: 1070
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_21208C.1
```

US-10-425-115-98353

Alignment Scores:

Pred. No.:	1,94e-101	Length:	1070
Score:	880.50	Matches:	163
Percent Similarity:	94.30%	Conservative:	19
Best Local Similarity:	84.46%	Mismatches:	10
Query Match:	88.23%	Indels:	1
DB:	8	Gaps:	1

US-10-688-481-11 (1-192) x US-10-425-115-98353 (1-1070)

```
Qy 1 MetPheLeuValAspTrpPheTYRGLYPheLeuAlaSerIleGlyLeuTrpGlnYsglu 20
Db 183 ATGTCTCGTGGACCTGCTTCTATGGGCTGCTGGCATCGCTTGGGCTGTGGCAAGAGAG 242
Qy 21 AlAlysIleLeuPheLeuGlyLeuAspAsnAlaGlyYsThrThrLeuLeuHISmetLeu 40
Db 243 GCTAAGATCCTCTCTCTGCTGCTGCAACGCGGCAAGACCACTCTTCACATGCTG 302
Qy 41 LysAspGluLysLeuGlyGlnHisGlnProThrGlnTrpProThrSerGluLeuSer 60
Db 303 AAGGACGAGCGGCTGTCAGACACGACGACGACGACGACGACGACGACGACGACGACG 362
Qy 61 IleAsnArgValIysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db 363 ATCGGACGATCAAGTTCAAGCGCTTGAACCTTGGGGCCACAGATCGCCCGCGCTC 422
Qy 81 TrpArgAspTrpTYRAlaLysValAspAlaIleValTYRLeuValAspAlaValAspArg 100
Db 423 TGGAGAGACTACTACGCGCAAGGTTGATGCTGTGTGTACTTGGTGTGATGCTGTGACAAG 482
Qy 101 GluArgPheAlaGlnSerIleYsgluLeuAspSerLeuSerAspAspSerLeuSer 120
Db 483 GAACGTTTCCGAGTCGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 542
Qy 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTYRAlaSerSerGluAsp 140
Db 543 AAGTTCCTTCTCTCACTGCGGCAACAGATTGACATCCCATACGCGGCTTCAGAGAG 602
Qy 141 GluLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyLysGlyThrValAsnLeu 159
Db 603 GAGCTGAGTACTACCTGCGGCTGAGCACTTCACACCGGGAAGGCAAGTGAACCTTG 662
Qy 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValAlaGlyMetGly 179
Db 663 GCGGATTCATATGTCGCGCCCTGAGAGATCTTCATGTGAGTGTGGCCCAAGATGGGC 722
Qy 180 TYRGLYGLUGLYPHELYSTRPMETTRHGINTRYILEYS 192
Db 723 TATGGCGAAGGCTTCAATGATGATCTCAGTACATCAAG 761

RESULT 9
US-10-425-115-98354
; Sequence 98354, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425, 115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 98354
; LENGTH: 1334
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_21209C.1
```


US-10-425-115-98354

Alignment Scores:	
Pred. No.:	2,678-101
Score:	880.50
Percent Similarity:	94.30%
Best Local Similarity:	84.46%
Query Match:	86.23%
DB:	8
Gaps:	1
Length:	133
Matches:	163
Conservative:	19
Mismatches:	10
Indels:	1

US-10-688-481-11 (1-192) X US-10-425-115-98354 (1-1334)

Oy 1 MetPheLeuValAspTyrPheTyrGlyPheLeuAlaSerTlGlyLeuTrpGlnTyrGln 20
 Db 271 ATGTTCCGTGGTGGACTGGTTCATAGGGGTCGTGGCATCCCTGGCTGTGGCAGAAAGAG 330
 Oy 21 AlaIysIleLeuPheLeuGlyLeuIspAenAlaGlyLysThrThrLeuLeuHisMetLeu 40
 Db 331 GCTAAGATCTCTCTTCCTGGCTCCGACCAAGCCGGAGAAACCACTCTCTCCACATGCTG 390
 Oy 41 LysAspGlyLysLeuGlyGlnHisGlnProThrGlnTyrProThreSerGlyLeuLeuSer 60
 Db 391 AAGGACGAGCGGCTGTACAGACCAAGCCGACCACTACCCACGTCAGAAAGTTGAGC 450
 Oy 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrTlIleAlaArgArgVal 80
 Db 451 ATCGCAGAGATCAAGTTCACAGGCGTTCCACTTTGGGGGGCCACCAAGTGGCCCGCCGCTC 510
 Oy 81 TyrArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
 Db 511 TGGAAAGACTACTAGCCCAAGGTGATGCTGTGTGTACTTGGTGTGATGCTGTGACAG 570
 Oy 101 GluArgPheAlaGlySerLysGlyLeuAspSerLeuLeuSerAspAspSerLeuSer 120
 Db 571 GAACCTTTTTCGCGAGTCGAGAAAGAGGCTTGATGCCCTTCTTGCAATGATCTCCCTTCA 630
 Oy 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
 Db 631 AAGCTTCTCTTCTCTACTACTGGGCAACAAGATTGAATCCCATACCGCGCTTCAGAGAG 690
 Oy 141 GluLeuArgPheThrLeuGlyLeuThr---MetThrThrGlyLysGlyThrValAsnLeu 159
 Db 691 GAGCTGAGAGTACTACTCGCGCTCGAGCAACTTCACAAACCGGAGAAAGGCAACGTGAACCTTG 750
 Oy 160 GlyAspSerSerAsnTlIleArgProIleGlyValPheMetCysSerTlIleValArgLysMetGly 179
 Db 751 GCCGACTCCAAATGTCGGGCCCCGCGAGATCTCATGTGAGTGTGGCGCAAGATGAGGC 810
 Oy 180 TyrGlyGlnGlyPheLysTrpMetThrGlnTyrTlIleLys 192
 Db 811 TATGGAGAAAGCTTCAAATGATGATGCTTCAGTACATCAAG 849

RESULT 10
ME-10-767

```

US-10-767-701-13805
/ Sequence 13805, Application US/10767701
/ Publication No. US20040172684A1
/ GENERAL INFORMATION:
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
/ FILE REFERENCE: 38-21(53535)B
/ CURRENT APPLICATION NUMBER: US/10/767,701
/ CURRENT FILING DATE: 2004-01-29
/ NUMBER OF SEQ. ID NOS: 63128
/ SEQ ID NO 13805
/ LENGTH: 954
/ TYPE: DNA
/ ORGANISM: Sorghum bicolor
/ FEATURE:
/ OTHER INFORMATION: Clone ID: SORBI-28WAY03-CLUS2820_1
US-10-767-701-13805

```

Alignment Scores:	
Pred. No.:	3,36e-101
Score:	877.50
Percent Similarity:	94.30
Best local Similarity:	84.46%
Query Match:	87.93%
DB:	7
Gaps:	1

US-10-688-481-11 (1-192) x US-10-767-701-13805 (1-954)

Oy 1 MetPheLeuValAlaSpTirPheTyrGlyPheLeuAlaSerIleGlyLeuTirPGLnlyVgLu 20
 Db 134 ATGTTCTCGTGGACTGGTTCTTACGGGGTGTGGCTCCGCTTGGCGCTGTGGCAAGAG 193
 Oy 21 AlaIyIleLeuPheLeuGlyLeuIbpaAnaIagIyLysThrThrLeuLeuHbMetLeu 40
 Db 194 GCGAAGATCTCTTCTCGGCTCGACACAAGCCGGAACACCACTCCCTCCACATCTTC 253
 Oy 41 LysAapGlyLysLeuGlyGlnIhIseGlnProThrGlnTyrProThrSerGlyLysLeuSer 60
 Db 254 AAGGACGAGCGGCTGTGCAGACACGCGACGACATACCCGACGTGAGAAGAGCTAGC 313
 Oy 61 IleAnaGValIysPheIysAlaPheAapLeuGlyGlyHisThrIleAlaArgVal 80
 Db 314 ATGGCAGAGATACAGTTCTTACAGGCTTCGACTCGGGGGCCACCAAGATCGCTCCGGGTC 373
 Oy 81 TrpAaspTyrTyrAlaIysValAspaIleValTyrIleuValAspaIvalAspaArg 100
 Db 374 TGGAAGATTACTTACGCAAAAGGTGATGCTGTAGTATACCTGTAGATGATATGACAAG 433
 Oy 101 GlnAapPheIagIuSerIysIysGlyLeuAapSerLeuLeuSerAapAapSerLeuSer 120
 Db 434 GAGCATTTGCGAATCAAAAAAGAGCTCGAAGCTCTCTGTGTATGATTTCTTGGCC 493
 Oy 121 GlnValProValIleuValIleuGlyAenIysIleAspIleProTyrAlaSerSerGluAap 140
 Db 494 AATGTTCATTTCTCTACTCTTGGCAACAAGATTGATATCCCATATGTGCTCTCGAAGAG 553
 Oy 141 GluLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyIysGlyThrValAsnLeu 159
 Db 554 GAGCTACGGTATCACCTAGCGCTTAGCAACTTACAAACCGGAAGGCAAGTCAACTT 613
 Oy 160 GlyAapSerAsnIleArgProIleGlyValPheMetCysSerIleValAlaGlyMetGly 179
 Db 614 GGTGACTCCAAATGTCGGGCACTTGAGGTTTCATGTGACAGTGTGTTCCCAAAATGGC 673
 Oy 180 TyrGlyGluGlyPheIysTirPheMetThrGlnTyrIleIys 192
 Db 674 TACGATGATGATTTCAAGTGGGCTCTCCCAATACATCAAG 712

RESULT 11

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: Sequence 45082, Application US/10437963
: Publication No. US20040123343A1
:
: GENERAL INFORMATION:
: APPLICANT: La Rosa, Thomas J.
: APPLICANT: Kovalic, David K.
: APPLICANT: Zhou, Yihua
: APPLICANT: Cao, Yongwei
: APPLICANT: Wu, Wei
: APPLICANT: Boukharov, Andrey A.
: APPLICANT: Bardazuk, Brad
: APPLICANT: Li, Ping
: TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
: FILE REFERENCE: 38-21(53221)B
: CURRENT FILING DATE: 2003-05-14
: NUMBER OF SEQ ID NOS: 204966
: SEQ ID NO 45082
: LENGTH: 1184
: TYPE: DNA
:

```



```

; ORGANISM: Oryza sativa
;
; FEATURE:
; OTHER INFORMATION: clone ID: PAT_MRT9530_48081C.1
US-10-437-963-45082

```

Alignment Scores:

Pred. No.:	2,35e+00	Length:	118
Score:	872.50	Matches:	161
Percent Similarity:	99.78	Conservative:	20
Best Local Similarity:	83.42	Mismatches:	11
Query Match:	87.42	Indels:	1
DB:	7	Gaps:	1

US-10-688-481-11 (1-192) X US-10-437-963-45082 (1-1184)

Oy 1 MetPheLeuValAspTTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnTyrGlu 20
 Db 148 ATGTTCTCTGGTTGACTGGCTTCTACGGGGGTCGTCGGCTCGCTGGGCTGTGGCAAGAGAG 207
 Oy 21 AlaIysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHisMetLeu 40
 Db 208 GCCAAGATCTCTTCTCTCGGCTCCGACCAAGCCGGGCAAGACCAACCTCTCCACATGCTC 267
 Oy 41 LysAspGlyLysLeuGlyGlnHisGlnProThrGlnTyrProThrsertGluLeuSer 60
 Db 268 AAGGACGAGCGGCTGTGTGACGACCAAGCCGAGCGACTACCCAGCTCGAGGAGGCTGAGC 327
 Oy 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
 Db 328 ATGGCAAGATCAAGATTCAAGGCTTTCGACTCTGGCGGCAACAGATCGCCGCGCGCTC 387
 Oy 81 TyrAspAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
 Db 388 TGGAAAGCACTACTACGCCCAAGGTCGATCTGTATTGTTACTTGGTGGATGCGGCTGCAAG 447
 Oy 101 GluArgPheAlaGluSerLysValysGluLeuAspSerLeuLeuSerLysAspSerLeuSer 120
 Db 448 GAACGCTTTCGCGAGTCGAAAGAAAGCTCGATGCTCTCTTCGCAACAGATTCCTCAGCA 507
 Oy 121 GluValProValLeuValLeuGlyLysLeuLysIleAspIleProTyrAlaSerSerGluAsp 140
 Db 508 ACCGTGCTCTTCTCTGATACTGCGGAAACAAGATCGACATCCCATCCCGCGCTCGAGGAG 567
 Oy 141 GluLeuArgPheThrLeuGlyLeuThr---MetThrThrGlyLysGlyThrThaLeuLeu 159
 Db 568 GAACCTCCGCTACTACTCTTGCTGTGAGCAACTTCACACCGGTAAAGGCAACGTGAACCTA 627
 Oy 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValAlnrgLysMetGly 179
 Db 628 GCCGCACTCAAGTCGCGGCTCTGGAGATCTTCATGTGACGCTCGTCCGCAAGATGGGC 687
 Oy 180 TyrGlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
 Db 688 TAGCGCAAGGCTTCAATGATGATGTCCCACTGATCAAA 726

```

, RESULT 12
, US-10-425-114-26805
, Sequence 26805, Application US/10425114
, Publication No. US20040034888A1
, GENERAL INFORMATION:
, APPLICANT: Liu, Jingdong
, APPLICANT: Zhou, Yihua
, APPLICANT: Kovalic, David K.
, APPLICANT: Screen, Steven E
, APPLICANT: Tabaska, Jack E
, APPLICANT: Cao, Yongwei
, TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
, TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
, FILE REFERENCE: 38-11(53313)B
, CURRENT APPLICATION NUMBER: US/10/425,114
, CURRENT FILING DATE: 2003-04-28
, NUMBER OF SEQ ID NOS: 73128
, SEQ ID NO 26805

```

```

; LENGTH: 1164
; TYPE: DNA
;
; ORGANISM: Zea mays
;
; FEATURE:
;
; OTHER INFORMATION: clone ID: LIB606-001-A8_FL1
US-10-425-114-26805

```

Alignment Scores:
Pred No.:

Pred. No.:	9,91e-100	Length:	1164
Score:	867.50	Matches:	161
Percent Similarity:	93.28%	Conservative:	19
Best Local Similarity:	83.44%	Mismatches:	12
Query Match:	86.92%	Indels:	1
DB:	7	Gaps:	1

US-10-688-481-11 (1-192) x US-10-425-114-26805 (1-1164)

QY 1 MetPheLeuValaApTTPheTTrpGlyPheLeuAlaSerIleAGLYLeuTrpGlnVal 20
 Db 259 ATGTTCTCGAGGACTGGATTCTATGGAGGTCTGGCAATCCCTTGGCTGGCAAGAGAG 318
 QY 21 AlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHisMetLeu 40
 Db 319 GCTAAGATCCTCTTCTTGGCTGCAACGCCGGCAAGACCACCTCTCCACATGCTG 378
 QY 41 LysAspGlnValbLeuGlyGlnHisbGlnProThrGlnTyrProThrSerGlnIleuSer 60
 Db 379 AAGCGACGCGGCTCGTACAGACACCGCGGACGAGTCCCACTCCACAGAGATTGAGC 438
 QY 61 IleAsnArgValbLysPheValaPheAspLeuGlyGlnHisThrIleAlaArgArgVal 80
 Db 439 ATCGCGAGGATCAAGTCAAGGCGTTCGACTTGGAGGCGCCGACACCGCGCGCGCTC 498
 QY 81 TrpArgAspTyrTyrAlaLysValaAspAlaIleValTyrLeuValaAspAlaValaAspArg 100
 Db 499 TGGAAAGCACTACAGCCAGAGTTGATGCTGTGTGTACTTGATGATGCTGTGTAAG 558
 QY 101 GlnArgPheAlaGlnSerIleValbGlnLeuAspSerLeuSerAspAspSerLeuSer 120
 Db 559 GAACCTTTGGCGAATCGAAGAGAGGCTTGATGGCTTCGCAATACATCCCTTCGCA 618
 QY 121 GlnValProValLeuValLeuGlyValAsnLysIleAspIleProTyrAlaSerSerGlnAsp 140
 Db 619 AACGTTCTCTTCTCATACTGGGCAACAAGATTGACATCCATACCGCGCTTCAGAGGAG 678
 QY 141 GlnLeuArgPheThrLeuGlyLeuThr--MetThrGlnTyrValbGlyThrValaLeuLeu 159
 Db 679 GAGCTGAGAGTACTACTCGGCTCGAGCAACTTCACACCGGGAAAGGCAACGTGAACCTTG 728
 QY 160 GlnAspSerAsnIleArgProIleGlnValPheMetCysSerIleValaArgLysMetGly 179
 Db 739 GCCGACTCCAAAGTCCGCCCTCGAAGATCTTCATGATGCAAGTGAGTGCGCAAGATGGC 798
 QY 180 TyrGlyGlnGlyPheLysTyrPheThrGlnTyrIleLys 192
 Db 799 TATGGCGAAGCTTCAATGCATGTCTCAAGTACATCAAG 837

```

RESULT 13
US-10-767-795-1304
; Sequence 1304, Application US/10767795
; Publication No. US2004018130A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53534)B
; CURRENT APPLICATION NUMBER: US/10/767,795
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 117596
; SEQ ID NO 1304
;
; LENGTH: 1047

```



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; TYPE: DNA
; ORGANISM: Goseypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-Cl800_1
US-10-767-795-1304

Alignment Scores:
Pred. No.: 2,05e-99 Length: 1047
Score: 864.50 Matches: 160
Percent Similarity: 93.78% Conservative: 21
Best Local Similarity: 82.90% Mismatches: 11
Query Match: 86.62% Indels: 1
DB: Gaps: 1

US-10-688-481-11 (1-192) x US-10-767-795-1304 (1-1047)
Qy 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnLeuGly 20
Db 221 ATGTTCTTGTGGATGGTCTTATGGTGTCTTCTGCTCCCTGGTCTATGGCAGAAAGAG 280
Qy 21 AlaIysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHISMetLeu 40
Db 281 GCTAAGATCTTGTCTTCGCTCGATACCCGCGCAAAACCACTTCTTCATATGTA 340
Qy 41 LysAspGluLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluLeuSer 60
Db 341 AAAGACGAGATGGTTCACATCAGCCCACTCAGTATCCACATCGAAGAGACTTAAT 400
Qy 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db 401 ATTGGAAATCAAGTTAAAGCTTTGATTTGGTGTCTCATGATTTGCTGTGAGTC 460
Qy 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db 461 TCGAAAGATTACTATGCTAAGGTGATGCTGTGATGCTGTATGATGCTATGATAA 520
Qy 101 GluArgPheAlaGluSerLysLysGluLeuAspSerLeuSerAspAspSerLeuSer 120
Db 521 GAGAGGTTTGCAAGATCGAAGAGAACTCGATCGCTTTCAGACGAGGCCCTTGCC 580
Qy 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
Db 581 AATGCCGCTTCTATCTCTAGAAACAAGATCGATATACATACGCTCGAGGAT 640
Qy 141 GluLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyLysGlyThrValAsnLeu 159
Db 641 GAATTACCTTACCATCTCGGCTCACAACCTTACCAAGCGGAGGAGGAGTGAACCTA 700
Qy 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGly 179
Db 701 GCAGACTCGAATGTCGCGCTGAGAGGTATTATGTCAGCATAGTCCGCAAAATGGGA 760
Qy 180 TyrGlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
Db 761 TATGGGACGGCTTTAAGTGATGTCTCATATATCAAG 799

RESULT 14
US-10-767-15389
; Sequence 15389, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5353)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 15389
; LENGTH: 928
; TYPE: DNA
```

```
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS49_287
US-10-767-701-15389

Alignment Scores:
Pred. No.: 3.09e-99 Length: 928
Score: 862.50 Matches: 159
Percent Similarity: 94.27% Conservative: 22
Best Local Similarity: 82.81% Mismatches: 10
Query Match: 86.42% Indels: 1
DB: Gaps: 1

US-10-688-481-11 (1-192) x US-10-767-701-15389 (1-928)
Qy 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnLeuGly 20
Db 154 ATGTTCTGTGAGCTGATCTACGGGCTGCTGCGCTCTGCGGCTGTGGCAGAAAGAG 213
Qy 21 AlaIysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHISMetLeu 40
Db 214 GCCAAGATCTTCTTCTCGGCTCGACCAAGCCGCGCAAGACCAAGCTCTCCACATGCTC 273
Qy 41 LysAspGluLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluLeuSer 60
Db 274 AAGGATGAGATTTGTCAGCATCAGCTTACACAGTATCCACTTCTGAAAGACTGAGC 333
Qy 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db 334 ATCGGAAGATCAAGATTCAAGGCACTTGTATGAGAGACATCAGATGCTCGCGGT 393
Qy 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db 394 TCGAAGGATTACTATGCTAAGGTGATGATGCTGATGCTTGTGATGCTTATGACAAAG 453
Qy 101 GluArgPheAlaGluSerLysLysGluLeuAspSerLeuSerAspAspSerLeuSer 120
Db 454 GAGCGGTTCTGTGATGTAAGAAAGAGCTAGATGCTCTCATGATGACTCCCTGACC 513
Qy 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
Db 514 ACTGCCCATCTTCGATCTCGGGAACAAGATCAATCCTTATGCGCTTCAAGAGAG 573
Qy 141 GluLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyLysGlyThrValAsnLeu 159
Db 574 GAATCCGTTATCAATCGGCTGAGCACTTACCACTGCGCAAGGCAAGTTAACTG 633
Qy 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGly 179
Db 634 GGCAGGCTTAACGTCCGCGCTGAGAGGTTCATGTGCAAGCGTTTGGCAAGATGGAG 693
Qy 180 TyrGlyGluGlyPheLysTrpMetThrGlnTyrIle 191
Db 694 TACGCCATGGGTTTAAGTGATGTCTCACAGTACATC 729

RESULT 15
US-10-425-114-20345
; Sequence 20345, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 20345
```


LENGTH: 986
TYPE: DNA
ORGANISM: *Zea mays*
FEATURE:
OTHER INFORMATION: Clone ID: L1B3180-039-D5_F11
-10-425-114-2045

Alignment Scores:

Seed. No.:	3.38e-99	986
Score:	862.50	160
Percent Similarity:	93.78%	21
Local Similarity:	82.90%	11
Very Match:	86.42%	1
3:	7	1
Gaps:		

5-10-688-481-11 (1-192) X US-10-425-114-20345 (1-986)

1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnLysGlu 20
130 ATGTTCTCTGGGACTGTTCTACGGGGTGCTGGCCCTCCCTGGCCCTGTGGCAGAGGAG 189

21 AlAysIleuPheluGlyLeuaspAsnIagIlystThrThrLeuHsiSmerIeu 40
|||
190 GCGAGATCTCTTCTCGGCTCGACACGCCGCGAAGACCAAGCTGTCCACATGCTC 249

41 LysAspGluLysLeuClgGlnHisGlnProThrGlnTyrProThrSerGlutIleValSer 60
|||:::|||||:::|||||
250 AAGCAGACGGCTTGTCAGCACCAAGCCGACGACGACACCACCGACGTGCGAGGAGCTCAGC 309

61 ILEasnArgValLysPheValAlaPheAspLeuGluTyrIleHisThrIleAlaArgArgVal 80
||| ::::::||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
310 ATGGCAAGATCAAGTTCAAGCCTTCGACCTCGGGCCGCACCAAGATCGCGGCCGCGTC 369

81 TTPAGASBPYYITVTAALYSVALASPATALEVAIIYILEUVALASPATLAVALSAPRIG 100
 |||::|||::|||::|||:

370 TGGAAGGATTACTACGCCAAGCTTGATGTCTAGTAACTCGTAGATGGCATGATAGAAG 429

D

430 GAGCATTTCGTAATCAAAAAGAGCTGACGCTCTCCTGCAGATGATTCCTTGCA 489

490 AATGTCATTCTCATCCCTGGCAACAGATTGATATCCCGATGCTGCTGAAAG 549

550 GAGCTGGCGGATACCTAGGCTTAGCAACTTCAACAACGGGAGGCAAGTCAACCTT 609

610 GGCGACTCCAATGTCGGCCACTTTGAGGTTTCATGTGCAGTGTGTTGCGAAGATGGGC 665

670 TACGGCGATGTTCAAGTGGGICTCCCAATACATCAAG 708

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search completed: December 9, 2005, 04:06:10
job time : 796 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 01:50:33 ; Search time 706 Seconds
(without alignments)
101.672 Million cell updates/sec

Title: US-10-688-481-11

Perfect score: 998
Sequence: 1 MFLVMFVGFSLSIGLMQKE.....STVRKMGYGEGRPMYQYIK 192

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlp
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-DB=Published Applications NA New -QMT=fastcap -SUFFIX=p2n.rmpbn -MINMATCH=0.1
-LONGLOG=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.csi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptco -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10688481_@CGN_1_184 @runat 05122005_094813_15941
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA New:

1: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	269.5	27.0	3891	US-10-955-054A-178	Sequence 178, App
2	248.5	24.9	2960	US-10-821-234-226	Sequence 226, App
3	221	22.1	591	US-11-093-746A-15	Sequence 15, Appl
4	221	22.1	3791	US-11-093-746A-1	Sequence 1, Appl
5	216.5	21.7	1650	US-10-821-234-76	Sequence 76, Appl
6	167	16.7	824	US-10-750-185-37034	Sequence 37034, A
7	167	16.7	2946	US-10-750-185-27986	Sequence 27986, A
8	165.5	16.6	746	US-11-099-691-26	Sequence 26, Appl

9	151.5	15.2	976	US-10-750-185-46137	Sequence 46137, A
10	130.5	13.1	678	US-10-750-185-28179	Sequence 28179, A
11	119.5	12.0	616	US-10-821-234-602	Sequence 602, App
12	99.5	10.0	2010	US-10-821-234-248	Sequence 248, App
13	97.5	9.8	1917	US-10-821-234-217	Sequence 217, App
14	90	9.0	2163	US-10-793-626-2057	Sequence 2057, App
15	90	9.0	3392	US-10-793-626-3396	Sequence 3396, App
16	89.5	9.0	1347	US-10-618-320A-27	Sequence 27, Appl
17	89.5	9.0	1353	US-10-618-320A-28	Sequence 28, Appl
18	89.5	9.0	1377	US-10-618-320A-2	Sequence 2, Appl
19	89	8.9	1365	US-11-112-944-3	Sequence 3, Appl
20	89	8.9	2631	US-11-074-176-321	Sequence 321, App
21	89	8.9	2649	US-11-074-176-87	Sequence 87, Appl
22	89	8.9	3128	US-10-821-234-831	Sequence 831, App
23	85.5	8.6	2005	US-10-821-234-531	Sequence 531, App
24	85	8.5	1185	US-10-821-234-774	Sequence 774, App
25	81.5	8.2	903	US-11-074-176-363	Sequence 361, App
26	81.5	8.2	924	US-11-074-176-253	Sequence 253, App
27	78.5	7.9	651	US-10-821-234-631	Sequence 631, App
28	78.5	7.9	1656	US-10-909-125-829	Sequence 829, App
29	78.5	7.9	134499	US-11-117-187-192	Sequence 192, App
30	76.5	7.7	1251	US-10-793-626-1461	Sequence 1461, App
31	76.5	7.7	3528	US-10-793-626-3791	Sequence 3791, App
32	76.5	7.7	171936	US-10-933-025-24	Sequence 24, Appl
33	76	7.6	753	US-11-055-822-1025	Sequence 1025, App
34	76	7.6	1997	US-10-750-185-29682	Sequence 29682, A
35	75.5	7.6	1062	US-11-060-023-3	Sequence 3, Appl
36	75.5	7.6	1062	US-11-060-023-5	Sequence 5, Appl
37	75.5	7.6	1062	US-11-060-023-7	Sequence 7, Appl
38	75.5	7.6	1080	US-11-060-023-1	Sequence 1, Appl
39	75	7.5	2324	US-10-821-234-4	Sequence 4, Appl
40	74.5	7.5	1128	US-11-060-023-9	Sequence 9, Appl
41	74.5	7.5	3669	US-11-186-284-174	Sequence 174, App
42	73	7.3	582	US-10-821-234-587	Sequence 587, App
43	73	7.3	2829	US-10-467-657-5507	Sequence 5507, App
44	73	7.3	328	US-10-467-657-5707	Sequence 5707, App
45	73	7.3	3337	US-10-793-626-3655	Sequence 3655, App

ALIGNMENTS

RESULT 1
US-10-955-054A-178
; Sequence 178, Application US/10955054A
; Publication No. US20050266420A1
; GENERAL INFORMATION:
; APPLICANT: PUSZTAI, LAJOS
; APPLICANT: SYMMANS, W. FRASER
; APPLICANT: HESS, KENNETH R.
; APPLICANT: AVERS, MARK
; TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
; FILE REFERENCE: VTXC:880US
; CURRENT APPLICATION NUMBER: US/10/955,054A
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 178
; LENGTH: 3891
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-955-054A-178

Alignment Scores:
Pred. No.: 2.76e-25
Score: 269.50
Percent Similarity: 33.18%
Best Local Similarity: 34.10%
Query Match: 27.00%
DB: 6
Gaps: 2
US-10-688-481-11 (1-192) x US-10-955-054A-178 (1-3891)

QY 19 LysGluAlaLysIleuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHis 38
Db 204 CAGAGGAGGAAATCTTCTCTCGCTGGATGATGCTGACAGACACTCTTCTGAAG 263
QY 39 MetLeuLysAspGlyLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluGlu 58
Db 264 CAGCTTGATGATGAGACATGACCAATCACACCTGACAGGGGTTTCACATCAAAAGT 323
QY 59 LeuSerIleAsnArgValLysPheLysAlaPheAspLeuGlyGlnHisThrIleAlaArg 78
Db 324 GTACAAATCAACAAGGTTTAAACCTGAATGTATGGGACATGCTGGACAGAGAAATCGA 383
QY 79 ArgValITPrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaVal 98
Db 384 CCATACCTGGAGAAATTTTGGAAATACCGATATCTTATATATGTAAATGACAGAGCA 443
QY 99 AspArgGluArgPheAlaGluSerLysLeuLeuAspSerLeuLeuSerAspAspSer 118
Db 444 GACGAAAAAAGATTTGAAGAGACCGGTCAGAACTAGCGGAATTTCTGAGAGAAAGAAA 503
QY 119 LeuSerGlnValProValIleuValIleuGlyAsnLysIleAspIleProTyrAlaSerSer 138
Db 504 CTAAGTGTGTGCGCAGTGTCTCATCTTGTATTAAGCAGATTTGCTCAGCAGCAGCCCT 563
QY 139 GluAspGluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyLysGlyThrValAsn 158
Db 564 GCCTCTGAAATTT-----GCAGAAAGG---CTGAAC 590
QY 159 LeuGlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMet 178
Db 591 CTGCATACCATCCGCGACCGAGTCTGGCAGATCCAGCTTCTCAGCTCTCAGCAGAGAG 650
QY 179 GlyTyrGlyGluGlyPheLysTyrPheThrGlnTyrIle 191
Db 651 GCGCTTCAGATGCGATGAGTGGGTCTGCAAAATATGTC 689

RESULT 2

US-10-821-234-226
; Sequence 226, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821.234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC_SEQ_Version 1.0
; SEQ ID NO 226
; LENGTH: 2960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-226

Alignment Scores:

Pred. No.: 1.29e-22 Length: 2960
Score: 248.50 Matches: 62
Percent Similarity: 47.94% Conservative: 31
Best Local Similarity: 31.96% Mismatches: 23
Query Match: 24.90% Indels: 7
DB: 6 Gaps: 4

US-10-688-481-11 (1-192) x US-10-821-234-226 (1-2960)

QY 3 LeuValAspTPrpPheTyrGlyPheLeuAlaSerIleGlyLeuTyrGlnLysGluAlaLys 22
Db 196 CTGCTGCACTGCTTCCTGCTC-----TTCTGGAAGAGAAATGAG 240

QY 23 IleuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHisMetLeuLysAsp 42
Db 241 CTGACGCTCTCGGGCTGCGAGTACTCGGCAAGCCACTTGTCAATGTCATCGCTCA 300
QY 43 GluLysLeuGlyGlnHisGlnProThrGlnTyrProThr-----SerGluGlu 58
Db 301 -----GCTCAATTCAGTAAAGATATGATACCCACAGTGGGCTTCAACATGAGAG 351
QY 59 LeuSerIleAsnArgValLysPheLysAlaPheAspLeuGlyGlnHisThrIleAlaArg 78
Db 352 GTAACTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 411
QY 79 ArgValITPrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaVal 98
Db 412 AGCATGGGAGGCGGTATTCAGAGAGTCAATGCTTGTATTAATGATGATGATGCA 471
QY 99 AspArgGluArgPheAlaGluSerLysLeuLeuAspSerLeuLeuSerAspAspSer 118
Db 472 GATGTAAAGATATGAAAGCTTCCGAAATGAGCTTATATATTTCTAGATTAACACAG 531
QY 119 LeuSerGlnValProValIleuValIleuGlyAsnLysIleAspIleProTyrAlaSerSer 138
Db 532 TTCAAGAAATTCAGAGTCTAGTCTTGGAAACAGAGAGATCTTCTAATGCTTGAT 591
QY 139 GluAspGluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyLysGlyThrValAsn 158
Db 592 GAGAAACAGCTA-----ATTGAAAAAATGAAAT 618
QY 159 LeuGlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMet 178
Db 619 CTGCTGCTATTCAGATGAGAAATTTGCTGCTATTCATTTCTTGCAGAAAGAAAGAT 678
QY 179 GlyTyrGlyGluGlyPheLysTyrPheThrGlnTyrIle 192
Db 679 AATATAGATATCAACATTCAGTGGCTTATTCAGATTCAAA 720

RESULT 3

US-11-093-746A-15
; Sequence 15, Application US/11093746A
; Publication No. US20050266443A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
; FILE REFERENCE: 3589.1015-003
; CURRENT APPLICATION NUMBER: US/11/093.746A
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: PCT/US2003/032270
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/417,842
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-093-746A-15

Alignment Scores:

Pred. No.: 6.3e-20 Length: 591
Score: 221.00 Matches: 54
Percent Similarity: 52.67% Conservative: 25
Best Local Similarity: 36.00% Mismatches: 57
Query Match: 22.14% Indels: 14
DB: 7 Gaps: 2

US-10-688-481-11 (1-192) x US-11-093-746A-15 (1-591)

QY 20 GluAlaLysIleuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHisMet 39
Db 34 GAAAGCCAGGTGATGATGAGCTGGACTCGGCGGCAAGACCAAGCTCTTCAAG 93


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Db 1127 AGATGACAGCATGCTGAAAAGATTTCAGAGAGTACGATGAGCTGCAGAAAAATGCTTCT 1068
Qy 115 rAspAspSerLeuSerGlnValProValLeuValLeuGlyValAsnValIleAspIleProTy 135
Db 1067 GGATGATGAAATTTGAGATGAGTGCCTGCTACTTTTGCAAAACAAGATTTGGCCAAA 1008
Qy 135 rAlaSerSerGlnAspGluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyValSgl 155
Db 1007 TGCTATGGCCATCATGAGTAAACAGATTAACATGAGGCTT----- 968
Qy 155 yThrValAsnLeuGlyAspSerAsnIleArgProIleGluValPheMetCysSerIleVal 175
Db 967 -----CAGTCTCTTCGTAACAAGAACTGATATGTTCAAGCCACTTG 927
Qy 175 lArgLyMetGlyTyTrGly-----GluGlyPheLeuTyTrMetThr 188
Db 926 TGCACAACAAGAACTGCTGTGTATGAAGACTTGACTGGCTGTCA 881

RESULT 6
US-10-750-185-37034/c
/ Sequence 37034, Application US/10750185
/ Publication No. US20050260603A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: FANTIN, Dennis
/ TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM11100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ PRIOR FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 37034
/ LENGTH: 824
/ TYPE: DNA
/ ORGANISM: Bovine 19866880402345
US-10-750-185-37034

Alignment Scores:
Pred. No.: 2,17e-12 Length: 824
Score: 167.00 Matches: 43
Percent Similarity: 50.00% Conservative: 23
Best Local Similarity: 32.58% Mismatches: 50
Query Match: 16.73% Indels: 16
Gaps: 4

US-10-688-481-11 (1-192) x US-10-750-185-37034 (1-824)
Qy 64 ValLySphelysAlaPheAspLeuGlyGlnHsThrIleAlaArgValTyTrAsp 83
Db 786 GTCCTGCTCAGCGCTGTGGAGCTTGAGACAGAAAGATGAGCCACCTGGGGCTC 727
Qy 84 TyTrAlaLyValAlaPheAlaIleValTyTrLeuValAspAlaValAspArgGluArgPhe 103
Db 726 TACTGTGAGAACTGATGAGCTGATGTATGTGTGGACATACAGACACACGACCTT 667
Qy 104 AlaGluSerLySglLeuAspSerLeuLeuSerLeuAspSerLeuSerGlnValPro 123
Db 666 GAAGACTCCAGAAAGATTGAGACATCTTGAAGAATGATGATTAATAAAGTGTGCT 607
Qy 124 ValLeuValLeuGlyAsnValIleAspIleProTyTrAla---SerSerGluAspGluLeu 142
Db 606 GTGCTCCTGTAGCCACAACAAGATATGCTGAGCTTAAGTCCGAGACATGACACC 547
Qy 143 ArgPheThrLeuGlyLeuThrMetThrThrGlySglTyTrValAsnLeuGlyAspSer 162
Db 546 AGGATGTTTC-----AAAGTGAAGCAACTCTGCGATGACCGG 511
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Qy 163 Asn-----IleArgProIleGluValPheMetCysSerIleValArgLyMetGlyTyTr 180
Db 510 AACTGTGCTGTGAGCC-----TGCTGTGCCCTCACTGGGAGACGGGCTA 466
Qy 181 GlyGluGlyPheLeuTyTrMetThrGlnTyTrIleLeu 192
Db 465 ATGAGGGGTTCCAGAAATTAACTGATTTGTGAAA 430

RESULT 7
US-10-750-185-27986/c
/ Sequence 27986, Application US/10750185
/ Publication No. US20050260603A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: FANTIN, Dennis
/ TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM11100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ PRIOR FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 27986
/ LENGTH: 2946
/ TYPE: DNA
/ ORGANISM: Bovine 19866880857076
US-10-750-185-27986

Alignment Scores:
Pred. No.: 1.44e-11 Length: 2946
Score: 167.00 Matches: 30
Percent Similarity: 86.67% Conservative: 9
Best Local Similarity: 66.67% Mismatches: 6
Query Match: 16.73% Indels: 0
Gaps: 0

US-10-688-481-11 (1-192) x US-10-750-185-27986 (1-2946)
Qy 14 lIleGlyLeuTrpGlnLySglValAlaLyIleLeuPheLeuGlyLeuAspAsnAlaGlyLyS 33
Db 147 TTAGGACTCTACACAGAAATCTGAAAACCTGTATCTTGGGTTTGACATTCAGGCGAAA 88
Qy 34 ThrThrLeuLeuHsMetLeuLySAspGluLyLeuGlyGlnHsGlnProThrGlnTyTr 53
Db 87 ACCACTCTTACACATGCTCAAAAGATGACAGACTGGGCGAGCATGTTCCAAAGTTACAT 28
Qy 54 ProThrSerGluGlu 58
Db 27 CCAAGTAGGTTTGA 13

RESULT 8
US-11-099-691-26
/ Sequence 26, Application US/11099691
/ Publication No. US20050260644A1
/ GENERAL INFORMATION:
/ APPLICANT: INCYTE PHARMACEUTICALS, INC.
/ APPLICANT: BANDMAN, Olga
/ APPLICANT: HITLMAN, Jennifer L.
/ APPLICANT: LAL, Preeti
/ APPLICANT: YUE, Henry
/ APPLICANT: TANG, Y. Tom
/ APPLICANT: PATTERSON, Chandra
/ APPLICANT: BAUGHN, Mariah R.
/ APPLICANT: YANG, Junming
/ TITLE OF INVENTION: CELL SIGNALING PROTEINS
/ FILE REFERENCE: PF-0521 PCT
```



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; CURRENT APPLICATION NUMBER: US/11/099,691
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US/09/700,444
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/085,343
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,010
; PRIOR FILING DATE: 1998-08-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PERL Program
; SEQ ID NO 26
; LENGTH: 746
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte Clone 3315936
; US-11-099-691-26

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Alignment Scores:
Pred. No.: 2,99e-12 Length: 746
Score: 165.50 Matches: 42
Percent Similarity: 54.48% Conservative: 31
Best Local Similarity: 31.34% Mismatches: 56
Query Match: 16.58% Indels: 5
Gaps: 3
US-10-688-481-11 (1-192) x US-11-099-691-26 (1-746)

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QY 18 GlnLysGlnAlaLysIleuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeu 37
Db 115 GAGAAAACAGCAAAATCTAGTGTGGCTGGATGAGCAAGAAACAGATGCTTG 174
QY 38 HMeMetLeuLysAspGlyLysLeuGlyGlnHisGln-----ProThrGlnTyrProThr 55
Db 175 CACTCTCTAGCTTCAACAGAGATC---CAGCACAGTGTGGCACCACCAAGGTTTCAT 231
QY 56 SerGlnGluSerIleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThr 75
Db 232 GCAGTTTGCATCAACACTGAGAGACGACGATGAGTCTCTGAGATTGTCGAGTAA 291
QY 76 IleAlaArgArgValTTPArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuVal 95
Db 292 CCTTTTGGTCTCTACTGGAAATGTACTTCAAGGAGTTGCTGCTGATCTTGTGTG 351
QY 96 AspAlaValAspArgGluArgPheAlaGlySerLysLysGluLeuAspSerLeuLeuSer 115
Db 352 GATTCAAGACATCAACAGCCGATTAACGAGCAAGAAATACCTTCATCAGTAATTGCA 411
QY 116 AspAspSerLeuSerGlnValProValLeuValLeuGlyLysLysIleAspIleProTyr 135
Db 412 GCAAAACCCAGTA-----CTTCTCTGTGGTGTGTTTGCACAAACAGATCTTGAAGCA 465
QY 136 AlaSerSerGluAspGluLeuArgPheThrLeuGlyLeuThr 149
Db 466 GCCTATCATCTACAGATATCATGAGCTTTGGCATTAATCT 507

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RESULT 9
US-10-750-185-46137
; Sequence 46137, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31

```

```

; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46137
; LENGTH: 976
; TYPE: DNA
; ORGANISM: Bovine
; US-10-750-185-46137

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Alignment Scores:
Pred. No.: 3.52e-10 Length: 976
Score: 151.50 Matches: 39
Percent Similarity: 46.88% Conservative: 21
Best Local Similarity: 30.47% Mismatches: 27
Query Match: 15.18% Indels: 41
Gaps: 4
US-10-688-481-11 (1-192) x US-10-750-185-46137 (1-976)

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QY 27 GlyLeuAspAsnAlaGlyLysThrThrLeuLysHMeMetLeuLysAspGlu----- 43
Db 609 GGCCTGACAAATGCCGCAAGACAGACATCTCAAGAGTTCAACCGTGAAGACATCGAC 668
QY 44 -----LysLeuGly--GlnHisGln----- 49
Db 669 ACCATCTCCCAACATGCGCTTCAACATCAAGACTTGAGACCGAGGTAAGCGGG 728
QY 50 -----ProThrGlnTyr----- 53
Db 729 TCCCGAGGCGCGCTGCCAGACAGGAGCGCGCGCGCGGCGGAGCTGACC 788
QY 54 -----ProThrSerGluGluLeuSerIleAsnArgValLysPheLysAlaPheAsp 71
Db 789 CTCGACCCCTCACT-----GCCCTGTCAGATTCAAGCTGAACATTGGAGT 836
QY 71 euGlyGlyHisThrIleAlaArgArgValTTPArgAspTyrTyrAlaLysValAspAlaI 91
Db 837 TGGCGCGCAAGAGTCCCTCGGCTCTACTGCGGAACTTCTTGAGAGACCGAGCGCC 896
QY 91 leValTyrLeuValAspAlaValAspArgGluArgPheAlaGlySerLysLysGluLeu 111
Db 897 TCATCTGGGTGGTGGACAGCGCGGACCGCAGCGCATGACAGACTGCGAGCGGAGCTCC 956
QY 111 spSerLeuLeuSerAspAsp 117
Db 957 AGAACCTGTTGTGTGAGAG 976

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RESULT 10
US-10-750-185-28179
; Sequence 28179, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28179
; LENGTH: 676
; TYPE: DNA
; ORGANISM: Bovine
; US-10-750-185-28179

```


Alignment Scores: 1.44e-07 Length: 676
Pred. No.: 130.50 Matches: 32
Score: 56.18% Conservative: 18
Percent Similarity: 35.96% Mismatches: 37
Best Local Similarity: 13.08% Indels: 2
Query Match: 6 Gaps: 1
DB: 1

US-10-688-481-11 (1-192) x US-10-750-185-28179 (1-676)

Qy 20 GlnAlaIysIleuPheLeuGlyLeuAspAsnAlaGlyIysThrThrLeuLeuHieMet 39
Db 405 GAAGCCCAAGGTGGATGATGAGCTGACTGCGCGGCAAGACCAAGCTCTTACAAA 464
Qy 40 LeuIysAspGlyIysLeuGlyGlnHisGlnProThrGlnIyrProThrSerGlnGluLeu 59
Db 465 CTGAAGGCCCAACAGCTGTGTGACACCTGCGCCACCGGTTCACAGTGAAGCCCTC 524
Qy 60 SerIle--AsnArgValIysPheLeuAlaPheAspLeuGlyGlyHisThrIleAlaArg 78
Db 525 GAGGCCCCCGGCGAGCTGTGCTCACCTCTGGATGTGCGGGGCGAGAGCCCACTCAG 584
Qy 79 ArgValTPArgAspIyrTyrrAlaIysAlaAspAlaIleValIyrLeuValAspAlaVal 98
Db 585 GCCAGCTGGAAGACTACTGAGAGGCGAGCCCTCTGTTGTGTGCTGACACACCA 644
Qy 99 Asp-ArgGlnuArgPheAlaGluSer 106
Db 645 GACGAGGGCCCGCTTGGCCGAGGCA 669

RESULT 11
US-10-821-234-602
; Sequence 602, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 602
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-602

Alignment Scores: 3.9e-06 Length: 618
Pred. No.: 119.50 Matches: 48
Score: 40.53% Conservative: 29
Percent Similarity: 25.25% Mismatches: 60
Best Local Similarity: 11.97% Indels: 53
Query Match: 6 Gaps: 10
DB: 1

US-10-688-481-11 (1-192) x US-10-821-234-602 (1-618)

Qy 22 LysIleuPheLeuGlyLeuAspAsnAlaGlyIysThrThrLeuLeuHieMetLeuLys 41
Db 37 AAGTACTTCTGATGGCACTCAAGGCTTGAAGTCTGCTCTCTTCAAGTTTGA 96
Qy 42 AspGlyIysLeuGlyGlnHisGlnProThrGlnIyrProThrSerGlnGluLeuSerIle 61
Db 97 GATGAT-----ACATATACGAAGAAGCTTACTC 123
Qy 62 AsnArgVal-----LysPheLeuAlaPheAspLeuGlyGlyHisThrIleAla 77

Db 124 AGCAAAATTGGTGTGATTTCAAAATAAGACATATAGATTAGACGGGAAAACATCAAG 183
Qy 78 ArgArgValTTP-----ArgAspIyrTyrr 85
Db 184 CTTCAAATATGGACACAGAGCCAGAGAAAGATTTGAAACATCATCCTTCAGATTATAC 243
Qy 86 AlaIysValAspAlaIleValIyrLeuValAspAlaValAspArgIynArgPheAlaGlu 105
Db 244 AGAGAGCCCATGGCATATAGTTGTATGATGACAGATCAAGAGTCCCTCAATTAAT 303
Qy 106 SerIys-----LysGluLeuAspSerLeuLeuSerAspAspSerLeuSerGlnVal 122
Db 304 GTTAAACAGTGGCTGACGAGAAATAGATCGTATGCCAGTGAAT-----GTC 351
Qy 123 ProValIleuValIleuGlyAsnIysIleAsp-----IleProTyrrAla 136
Db 352 AACAAATTTGTATGAGGAACAAATGTATCTGACCAAAAGAAAGTAGAGCTACACA 411
Qy 137 SerSerGluAspGluLeuArgPheThrLeuGlyLeuThrMet-----ThrThrGlyLys 154
Db 412 ACAGCGAAG--GAATTGCTGATTCCTTGAATTCCGTTTGGAAACAGTGTCTAAG 468
Qy 155 GlyThrValAsnLeuGlyAspSerAsnIleArgProIleGluValPheMet----- 171
Db 469 AATGCAACGATGTAGAACATCT-----TTCAATGACGATGCGA 507
Qy 172 CysSerIleValArgLysMetGlyTyrrGly 181
Db 508 CGTGAGATTAAAGCAAGCAATGGTCCCGGA 537

RESULT 12
US-10-821-234-248
; Sequence 248, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 248
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-248

Alignment Scores: 0.0116 Length: 2010
Pred. No.: 99.50 Matches: 31
Score: 42.73% Conservative: 16
Percent Similarity: 28.18% Mismatches: 25
Best Local Similarity: 9.97% Indels: 3
Query Match: 6 Gaps: 3
DB: 1

US-10-688-481-11 (1-192) x US-10-821-234-248 (1-2010)

Qy 49 GlnProThrGlnIyrProThrSerGlnGluLeuSerIleAsnArgValLys----- 65
Db 653 CAGAGTACTTACATCCACACAGAAAGATGTGCTACGAGCCCGTAAAGACCAAGGGG 712
Qy 66 -----PheIysAlaPheAspLeuGlyGly 73
Db 713 ATCGTGAGACACACTTCAACCTTCAAGACCTTCAAGATGTTGATGTGGGTGGT 772
Qy 74 HisThrIleAlaArgArgValTTPArgAspIyrTyrrAlaIysValAspAlaIleValIyr 93


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Db 773 CACGGCTGTGAGCGAAGAGTGCATCTGCTTGGAGCGCTCACAGCATCATCTTC 832
Qy 94 -----leuValAspAlaValAspArgIu-----ArgPhe 103
Db 833 TGGCTAGCCTTGAGCCGCTATGACTGTGCTAGCTAGAGCAGATGAACCGCATG 892
Qy 104 AlaGluSerIysGluLeuAspSerLeuSerAspAspSerLeuSerGlnValPro 123
Db 893 CAGGAGGACATGAAGCATTCGATAGCATCTGCACAACAAGTGTTCAAGACAGCTCC 952
Qy 124 ValIeuValIeuGlnIysAsnIysIleAspIle 133
Db 953 ATCATCTCTTCTCTCAACAGAGAGACCTG 982

RESULT 13
US-10-821-234-217
; Sequence 217, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PL_SEQ_Version 1.0
; SEQ ID NO 217
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-217

Alignment Scores:
Pred. No.: 0.0202 Length: 1917
Score: 97.50 Matches: 45
Percent Similarity: 38.71% Conservative: 27
Best Local Similarity: 24.19% Mismatches: 70
Query Match: 9.77% Indels: 45
DB: 6 Gaps: 7

US-10-688-481-11 (1-192) x US-10-821-234-217 (1-1917)
Qy 22 LysIleuPheLeuGlnIysLeuAspAsnAlaGlyIysThrThrLeuLeuHisMetLeuLys 41
Db 75 AACCTGCTTTGATGGCGACTCAGCGGTGGCGAAGTCATGCTGCTCCGCGTTGCT 134
Qy 42 AspGlnIysLeuGlnIysGlnProThrGlnIysProThrSerGlnIysLeuSerIle 61
Db 135 GATGAC-----ACGTACACAGAGAGCTATC 161
Qy 62 AsnArgVal-----LysPheLysAlaPheAspLeuGlnIysIleThrIleAla 77
Db 162 AGCACCATCGGGGTGACCTTCAGATCCAGACATCGAGCTGATGGCAAACTATCMAA 221
Qy 78 ArgArgValTrp-----ArgAspIysIysIle 85
Db 222 CTTCAAGATCTGGACACAGCGGGCCAGAACGGTTCGGACATCACTTCCAGCTACTAC 281
Qy 86 AlaLysValAspAlaIleValIysLeuValAspAlaValAspArgIuArgPheAlaGlu 105
Db 282 CGGGGGGCTCATGGCATCATCGTGTATGACGTCACTGACCAAGAACTCTAGCGCAAC 341
Qy 106 SerIysIysGlnLeuAspSerLeuSerAspAspSerLeuSerGlnValProValIeu 125
Db 342 GTGAAGCAAGTGGCTGACGAGGAGATTCACCGCTAT-GCCAGCGAGAACGTCAATAAGCTC 400
Qy 126 ValIeuGlnIysAsnIysIleAspIleProIysAlaSerSerGlnAsp----- 140
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Db 401 CTGTGGGCAACAAGAGCAGCTCACACCAAGAGGTGTGACAACAACACAGCCAG 460
Qy 141 GlnLeuAspPheThrLeuGlnIysLeuThrMet-----ThrThrIysGlnIysThrValAsn 158
Db 461 GAGTTTGACAGACTCTTGGGCAATCCCTCTTGGAGACGACGCGCAAGAAATGCCACCAAT 520
Qy 159 LeuGlyAspSerAsnIleAspProIleGlnValPheMet-----CysSerIleVal 175
Db 521 GTCGAG-----CAGGCTTATATACATGAGCTGCTGAATAATCAA 559
Qy 176 ArgIysMetGlyIysIle 181
Db 560 AAGCGATGGGGCCTGGA 577

RESULT 14
US-10-793-626-2057
; Sequence 2057, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2057
; LENGTH: 2163
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-2057

Alignment Scores:
Pred. No.: 0.251 Length: 2163
Score: 90.00 Matches: 33
Percent Similarity: 48.00% Conservative: 27
Best Local Similarity: 26.40% Mismatches: 57
Query Match: 9.02% Indels: 8
DB: 6 Gaps: 3

US-10-688-481-11 (1-192) x US-10-793-626-2057 (1-2163)
Qy 18 GlnLysGlnAlaLysIleLeuPheLeuGlnIysLeuAspAsnAlaGlyIysThrThrLeuLeu 37
Db 664 GAACTGCAGACGATTTTACATCATGGGCGACGTAAGCATGTAAGCATTTATTA 723
Qy 38 HisMetLeuLysAspGlnIysLeuGlnIysGlnPro-----ThrGlnIysPro 54
Db 724 GATTCTATTTCGTAACTAAAGTTACAGAGAGAGAGAGTGGCGGAATCACTCAACATATT 783
Qy 55 ThrSerGlnIysLeuSerIleAsnArgValIysPheLysAlaPheAspLeuGlnIysHis 74
Db 784 GGTGCTTATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 843
Qy 75 ThrIleAlaArgArgValTrpArgAspIysIysIleValAspAlaIleValIysLeu 94
Db 844 GCT--GCAATTTACGACTATGCTGACGCTGCTGCTCAAGTTACTGATATTACAAATTTTA 900
Qy 95 ValAspAlaValAspArgIuArgPheAlaGluSerIysIysGlnLeuAspSerLeu 114
Db 901 GTGCGGCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Qy 115 SerAspAspSerLeuSerGlnValProValIeuValIeuGlnIysAsnIysIleAspIlePro 134
Db 961 GAA-----GCAAGATACCTACGATTTGACGATTAACAAATAATGATTAACCA 1008
Qy 135 TyrAlaSerSerGln 139
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Db 1009 ACTGCTAACCTGAT 1023

RESULT 15

US-10-793-626-3396/c
; Sequence 3396, Application US/107933626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUI480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3396
; LENGTH: 3792
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3396

Alignment Scores:

Pred. No.:	0.578	Length:	3792
Score:	90.00	Matches:	33
Percent Similarity:	48.00%	Conservative:	27
Best Local Similarity:	26.40%	Mismatches:	57
Query Match:	9.02%	Indels:	8
DB:	6	Gaps:	3

US-10-688-481-11 (1-192) x US-10-793-626-3396 (1-3792)

QY 18 GlnlyseGluAlaLysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeu 37
Db 3290 GAACGTCGACGAGTTGATACATCATGGCCACGATGATGTTAAACGACTTTATTA 3231
QY 38 HistetleuLysAspGluLysLeuGlyGlnHisGlnPro-----ThrGlnTyPro 54
Db 3230 GATTCTATTGTAACACTAAAGTTACAGAGAGAGCTGGCGGAATCATCTCAACATATT 3171
QY 55 ThrSerGluGluLeuSerIleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHis 74
Db 3170 GGTGCTTATCAAAATTGAATAATTCAGTAAATAATTACGTTCTTAGATACCTCGACAT 3111
QY 75 ThrIleAlaArgArgValTrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeu 94
Db 3110 GCT---GCATTATACGACTATGCGTGCACGTGCTCAAGTTACTGATATTACAATTTTA 3054
QY 95 ValAspAlaValAspArgGluArgPheAlaGluSerLysLysGluLeuAspSerLeuLeu 114
Db 3053 GTCTGGCCGCTGATGATGCTGTGATGCTCAACAAATTGAAGCTATTAATCAGCTAAA 2994
QY 115 SerAspAspSerLeuSerGlnValProValIleuValLeuGlyAsnLysIleAspIlePro 134
Db 2993 GAA-----GCAGAACTACTTACGATTGTTGCACTAAACAAAATTGATTAACCA 2946
QY 135 TyrAlaSerSerGlu 139
Db 2945 ACTGCTAACCTGAT 2931

Search completed: December 9, 2005, 04:18:09
Job time : 711 secs